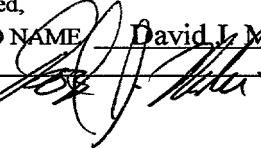


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UTILITY PATENT APPLICATION TRANSMITTAL		Attorney Docket No. 210121.428C3
		First Inventor or Application Identifier Jiangchun Xu
Title		COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE
(Only for nonprovisional applications under 37 CFR § 1.53(b))		Express Mail Label No. EM175835678US
APPLICATION ELEMENTS <i>See MPEP chapter 600 concerning utility patent application contents.</i>		ADDRESS TO: Box Patent Application Assistant Commissioner for Patents Washington, D.C. 20231
<p>1. <input checked="" type="checkbox"/> General Authorization Form (Submit an original and a duplicate for fee processing)</p> <p>2. <input checked="" type="checkbox"/> Specification [Total Pages] 134 (preferred arrangement set forth below)</p> <ul style="list-style-type: none"> - Descriptive Title of the Invention - Cross References to Related Applications - Statement Regarding Fed sponsored R & D - Reference to Microfiche Appendix - Background of the Invention - Brief Summary of the Invention - Brief Description of the Drawings (if filed) - Detailed Description - Claim(s) - Abstract of the Disclosure <p>3. <input type="checkbox"/> Drawing(s) (35 USC 113) [Total Sheets]</p> <p>4. Oath or Declaration [Total Pages]</p> <ul style="list-style-type: none"> a. <input type="checkbox"/> Newly executed (original or copy) b. <input type="checkbox"/> Copy from a prior application (37 CFR 1.63(d)) (for continuation/divisional with Box 17 completed) <ul style="list-style-type: none"> i. <input type="checkbox"/> DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b) <p>5. Incorporation By Reference (useable if box 4b is checked) The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.</p> <p>6. <input type="checkbox"/> Microfiche Computer Program (Appendix)</p> <p>7. Nucleotide and Amino Acid Sequence Submission (if applicable, all necessary)</p> <ul style="list-style-type: none"> a. <input checked="" type="checkbox"/> Computer-Readable Copy b. <input checked="" type="checkbox"/> Paper Copy (identical to computer copy) c. <input checked="" type="checkbox"/> Statement verifying identity of above copies 		
ACCOMPANYING APPLICATION PARTS		
<p>8. <input type="checkbox"/> Assignment Papers (cover sheet & document(s))</p> <p>9. <input type="checkbox"/> 37 CFR 3.73(b) Statement (when there is an assignee) <input type="checkbox"/> Power of Attorney</p> <p>10. <input type="checkbox"/> English Translation Document (if applicable)</p> <p>11. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations</p> <p>12. <input type="checkbox"/> Preliminary Amendment</p> <p>13. <input checked="" type="checkbox"/> Return Receipt Postcard</p> <p>14. <input type="checkbox"/> Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired</p> <p>15. <input type="checkbox"/> Certified Copy of Priority Document(s) (if foreign priority is claimed)</p> <p>16. <input checked="" type="checkbox"/> Other: <u>Certificate of Express Mail</u> _____ _____</p>		
<p>17. If a CONTINUING APPLICATION, check appropriate box and supply the requisite information below and in a preliminary amendment</p> <p><input type="checkbox"/> Continuation <input type="checkbox"/> Divisional <input checked="" type="checkbox"/> Continuation-In-Part (CIP) of prior Application No.: <u>Not Available</u></p> <p>Prior application information: Examiner _____ Group / Art Unit _____</p> <p><input type="checkbox"/> Claims the benefit of Provisional Application No. _____</p>		
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Respectfully submitted,

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

REFERENCE TO RELATED APPLICATIONS

5 This application is a continuation-in-part of U.S. Patent Application No. _____, filed February 9, 1998 (Attorney Docket No. 210121.428C2), which is a continuation-in-part of U.S. Patent Application No. 08/904,809, filed August 1, 1997, which is a continuation-in-part of U.S. Patent Application No. 08/806,596, filed February 25, 1997.

10

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for 15 the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with 20 an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the 25 disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited 30 diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA

measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

5

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of 10 said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and 15 monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds 20 to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above 25 polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as 30 diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that
5 encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177
10 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a
15 DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: : 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide
20 probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

25

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion
30 of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants

preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating
5 the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

10 As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu,
15 asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

20 Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a
25 polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for
30 example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and

most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; 5 followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate 10 tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA 15 molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 20 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence 25 encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 30 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase

techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems 5 Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of 10 expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells 15 employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are 20 homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods 25 disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker 30 peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA

sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA
5 translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into
10 the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and
15 (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent
20 No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable
25 transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

30 Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention

may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described herein. In other words, antibodies or other binding
5 agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins
10 are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length
15 protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate
20 tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that
25 binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in
30 combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate

cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include
5 blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent
10 association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant
15 is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

20 Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized.
25 Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory,
30 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second

binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the 5 binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be 10 a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support 15 using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). 20 Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or 25 polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with 30 both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an

aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.

5 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a
10 different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically
15 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact
20 time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide.
25 Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second
30 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and

biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide.

- 5 An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally
- 10 appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction
- 15 products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or

to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or
5 strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody
10 may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the
15 concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in
20 the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use
25 with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the
30 level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of

polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding

activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in

chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described 5 in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody 10 portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a 15 photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one 20 embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for 25 attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may 30 also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating

compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For 5 example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the 10 precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a 15 polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a 20 DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, 25 preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected 30 from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided

in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, 5 prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for 10 using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. 15 Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a 20 pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic 25 galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain 30 DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in

the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*)
5 that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y.*
10 *Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994;
15 Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be
20 increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and
25 vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients.
30 A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In

general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to 5 about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a 10 lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable 15 microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of 20 immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment 25 of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of 30 the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-

specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by
5 way of limitation.

EXAMPLES

EXAMPLE 1

10 ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from
15 prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA
20 was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns
25 (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA
30 libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64 x 10⁷ independent colonies, with 70% of

clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence
5 and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted
10 cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As
15 recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was
20 digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The
25 sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol
30

resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1.

To analyze the subtracted cDNA library, plasmid DNA was prepared
5 from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be
10 abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known
15 sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously
20 identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

25 To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase
30 subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second

subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for 5 the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, 10 N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to 15 be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 20 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 25 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by 30 subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-

3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was
5 performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-
10 3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and
15 prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described
20 above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807,
25 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766,
30 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated

clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

5

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17

and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal

prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

10 ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR
POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, 15 placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was 20 isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, 25 P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of 30 these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were

found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to 5 previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences 10 being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, 15 kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate 20 tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was 25 found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For 30 P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal

PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5)
5 compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of sixteen additional clones. The determined DNA sequences for these clones are provided in SEQ ID NO: 207-222.

10

EXAMPLE 4 SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A
15 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture:
20 trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to
25 elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific
30 embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Seattle
- (D) STATE: WA
- (E) COUNTRY: USA
- (F) ZIP: 98104

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 23-FEB-1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Maki, David J.
- (B) REGISTRATION NUMBER: 31,392
- (C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (206) 622-4900
- (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC	60
ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT	120
CCAGGGGGTC CAGTCCCTCT CCTTACTTCA TCCCCATCCC ATGCCAAAGG AAGACCTCC	180
CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCCTC CAGGACAGAG TGGTTATGT	240

TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTGTT	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTG	GAAATTGTTA	TCCGCTCACCA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTGCGCTCA	CTGNCCGCTT	TCCAGTCNNG	AAAACGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGAAAAA	GCGGTTTGCG	TTTTGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNNG	AAAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGA	120
CTAAAGTCTG	ATGAACTTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTGTC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAAC	300
AAGGAACGGG	GCTCGTTAT	CACCAGTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGACACCT	360
CTGCTGTTAA	ACACCCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCCCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTGCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAAACGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGNC	CCGGTCTTCG	GCTGCNNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNNTNCCGG	TTATCCCCAA	ACNGGGATA	CCCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCAGC	60
TCCTGCTCCT	CACTGGTGT	AAACGAGCCC	CGTTCTTGT	TGTGATCATG	ATGAACAACC	120
TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTG	CGTCAAAGAT	TTGACACCCAC	180
TCTGCCCTCG	TCTTCTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTGCGC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480

GTGACTGGGA AAACCCTGGG CGTTACCAAC TTAATCGCCT TGCAGCACAT CCCCCTTCG	540
CCAGCTGGC GTAATANCNA AAAGGCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT	600
GAATGGGNAATGGGACCCCC CCTGTTACCG CGCATTNAAC CCCCNGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTGCCA GCGCCTTANC GCCCGCTCCC TTTCNCCCTT	720
CTTCCCTTCC TTTCNCCCN CTTTCCCCCG GGGTTCCCC CNTCAAACCC CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT CCTACTGACC TGTGCTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG	60
AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTC GTCCTCTCCT	120
TCGAACACT GGCTGCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG	180
ACGTGGGTGA CCATGTTGTT TGTGGGGTGC AGAGATGGGA GGGGTGGGGC CCACCTGGA	240
AGAGTGGACA GTGACACAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC	300
ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCT	360
GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAG AAGGGGAGGA TCCACTAGTT	420
CTANAGCGGC CGCCACCGCG GTGGANCTCC ANCTTTGTT CCCTTTAGTG AGGGTTAATT	480
GCGCGCTTGG CNTAACATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA	540
ATTCACACACA ACATACGANC CGAAACATA AANTGTAAAC CTGGGGTGCC TAATGANTGA	600
CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCCCTTTC CAATCNGGAA ACCTGTCTTG	660
CCNCCTGCAT TNATGAATCN GCCAACCCCC GGGGAAAAGC GTTTGCCTTT TGGCGCTCT	720
TCCGCTTCCCT CNCTCANTTA NTCCCTNCNC TCGGTCTATT CGGCTGCNGC AAACCGGTTTC	780
ACNCCTCCA AAGGGGTAT TCCGGTTTCC CCNAATCCGG GGANANCC	828

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT	60
AGTTTTAATT GCATCAAAG TACTAACAA AACTCTAGCA ATCAAGAATG GCAGCATGTT	120
ATTTTATAAC AATCAACACC TGTTGCTTT AAAATTGGT TTTCATAAGA TAATTTATAC	180
TGAAGTAAAT CTAGCCATGC TTTAAAAAA TGCTTAGGT CACTCCAAGC TTGGCAGTTA	240
ACATTTGGCA TAAACATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATACAG TATAAGAAA AGGTGGTAGT GTTGTAGTAAG CAGTTATTAG	360
AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTGATTCA TCAGCCCTGA	420
CATTCAAGTT TCAAAGTAGG AGACAGGTT TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTC AAGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTTAAA TTAGTGTCAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT	660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGA ACTGGAACAT	720
TGNATNACAG TGTCCANAG TTNAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780

TGTTATTTG TTAAAAATTA AATTAAACC TGGTGGAAAA ATAATTTGAA ATNA 834

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT	TTTTTTTTTT	AAGACCCCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTGGA	120
TGTAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAAATGTT	GAGCCGTAGA	TGCCGTGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	AAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGC	CTANTATGAA	GAACTTTGG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAA	GGCCCTGTTA	NGGGTCTGGG	CTNGGTTTA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT	TTTTTTTTTT	TGGCTCTAGA	GGGGTAGAG	GGGGTGTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTTAGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCCTCC	ACAGATTTC	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTTG	GTTCAGACGT	CCGGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTA	TTATTATACN	AATGGGGCT	TCAATCGGGA	300
GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTCGCC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GAATGAAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCTAG	GTTCAATACC	420
ATTGGTGGCC	AATTGATTTG	ATGGTAAGGG	GAGGGATCGT	TGAACTCGTC	TGTTATGTA	480
AGGATNCCTT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCGG	GCANGATATT	540
TCAAACNGTC	TCTANTCCT	GAAACGTCTG	AAATGTTAAT	AAAATTAAN	TTTNGTTATT	600
GAATNTTNNG	GAAGAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGTNATA	ACCNCTCTA	TNATCCCACC	CAATNGNATT	CCCCACNCNN	720
ACNATTGGAT	NCCCCANTTC	CANAAANGGC	CNCCCCCGG	TGNANNCCNC	CTTTGTTCC	780
CTTNAATGAN	GGTTATTTCNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACAAGC	GGGAGAGCGA	CTCCGAGCGT	120
CTGAAGCGCA	CGTCCCAGAA	GGTGGACTTG	GCACTGAAAC	AGCTGGGACA	CATCCGCGAG	180
TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCAGC	AGTGTAGCG	CGTCCTGGGG	240
TGGGTGGCCG	ANGCCTGANC	CGCTCTGCCT	TGCTCCCCC	ANGTGGGCG	CCACCCCCCTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTGC	TGGCGACTT	CAAGGANAAC	CCCCACANGG	360
GGATTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCCACCTG	GTTGCCCTTG	420
TCTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCNG	GACCACCTT	NGGGAGTGT	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNNT	NCTANAACCG	GCCNCNCNC	CNGTGGAAACC	CNCCTTNTGT	600
TCCTTTCTNT	TNAGGGTTAA	TNNCGCCTTG	GCCTTNCCAN	NGTCCTNCNC	NTTTTCCNNNT	660
GTTNAATTG	TTANGCNCCC	NCCNNNTCCCN	CNNCNCCNAN	CCCGACCCNN	ANNTNNNANN	720
NCCTGGGGGT	NCCNNCNGAT	TGACCCNNCC	NCCCTNTANT	TGCNTTNGGG	NNCNTGCC	780
CTTCCCTCT	NGGGANNCG					799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT	CCTCCCAGGC	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTTG	60
TAANGATGAC	ACTCCCCAAG	GTGGTCCTGA	CAGTGGCCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAGGT	GCGGGGGCCG	AAGCCACAT	GATCCTTACT	CTATGAGCAA	180
AATCCCCTGT	GGGGGCTTCT	CCTTGAAGTC	CGCCANCAGG	GTCAGTCTT	TGGACCCANG	240
CAGGTCACTGG	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGGCNCA	GGGCTCNGN	300
CACCCATCCC	ANGACGGGC	TACACTNCTG	GACCTCCNC	TCCACCACCT	TCATGCGCTG	360
TTCNTACCCG	CGNATNTGTC	CCANCTGTTT	CNGTGCCNAC	TCCANCTTCT	NGGACGTGCG	420
CTACATACGC	CCGGANTCNC	NCTCCCGCTT	TGTCCTTATC	CACGTNCCAN	CAACAAATT	480
CNCCNTANTG	CACCNATTCC	CACNTTNNNC	AGNTTCCNC	NNCGNGCTTC	CTTNAAAAG	540
GGTGANCCCC	CGGAAAATNC	CCCAAAGGGG	GGGGGCCNGG	TACCCAACTN	CCCCCTNATA	600
GCTGAANTCC	CCATNACNN	GNCTCNATGG	ANCCNTCCNT	TTTAANNACN	TTCTNAACTT	660
GGGAANANCC	CTCGNCCNTN	CCCCNNTAA	TCCCNCTTG	CNANGNNCNT	CCCCCNNTCC	720
NCCNNNTNG	GCNTNTNANN	CNAAAAAGGC	CCNNNANCAA	TCTCCTNNCN	CCTCANTTCG	780
CCANCCCTCG	AAATCGGCCN	C				801

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT	GGCCAGTGTG	GCAGCTTTCC	CTGTGGCTGC	CGGTGCCACA	TGCCTGTCCC	60
ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	GTTCACCTTC	TCAGCCCTGC	120
AGATCCTGCC	CTACACACTG	GCTCTCCCTCT	ACCACCGGGA	GAAGCAGGTG	TTCCTGCCCA	180
AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	CCTGATGACC	AGCTTCCTGC	240
CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	GGGTGCTGGA	GGCAGTGGCC	300
TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	TGATGTCTCC	GTACGTGTGG	360
TGGTGGGTGA	GCCCACCGAN	GCCAGGGTGG	TTCCGGGCCG	GGGCATCTGC	CTGGACCTCG	420
CCATCCTGGA	TAGTGTCTCC	TGCTGTCCCA	NGTGGCCCCA	TCCCTGTTA	TGGGCTCCAT	480
TGTCAGCTC	AGCCAGTCTG	TCACTGCCTA	TATGGTGTCT	GCCGCAGGCC	TGGGTCTGGT	540
CCCATTACT	TTGCTACACA	GGTANTATT	GACAAGAACG	ANTTGGCCAA	ATACTCAGCG	600
TTAAAAAAATT	CCAGCAACAT	TGGGGGTGGA	AGGCCTGCCT	CACTGGGTCC	AACTCCCCGC	660
TCCTGTTAAC	CCCATGGGC	TGCCGGCTTG	GCCGCCAATT	TCTGTTGCTG	CCAAANTNAT	720
GTGGCTCTCT	GCTGCCACCT	GTTGCTGGCT	GAAGTGCNTA	CNGNCNANCNT	NGGGGGGTNG	780
GGNGTTCCC						789

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC	CCAAATATTA	GACACCAACA	CAGAAAAGCT	AGCAATGGAT	TCCCTTCTAC	60
TTTGTAAAT	AAATAAGTTA	AATATTTAAA	TGCCCTGTGTC	TCTGTGATGG	CAACAGAAGG	120
ACCAACAGGC	CACATCTGA	TAAAAGGTAA	GAGGGGGGTG	GATCAGCAAA	AAGACAGTGC	180
TGTGGGCTGA	GGGGACTCTGG	TTCTTGTGTC	TTGCCCTCA	GGACTCTTCC	CCTACAAATA	240
ACTTTCATAT	GTTCAAATCC	CATGGAGGAG	TGTTTCATCC	TAGAAACTCC	CATGCAAGAG	300
CTACATTAAA	CGAAGCTGCA	GGTTAAGGGG	CTTANAGATG	GGAAACCAGG	TGACTGAGTT	360
TATTTCAGCTC	CCAAAACCC	TTCTCTAGGT	GTGTCTAAC	TAGGAGGCTA	GCTGTTAACCC	420
CTGAGCCTGG	GTAATCCACC	TGCAAGAGTC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTAACAA	600
GCACAGGGTG	GCAGAAAAAA	AACCACTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTAAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAATNTT	GCTGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCTC	TACTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATA	TTGGTGAAGC	CACAGCAC	GAGCCCTTC	240
ATGGTGGTGT	TCCACACTG	AGTGAAGTCT	TCCTGGAAC	CATAATCTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCNA	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCCTGCN	TNGTGGCTCC	TGTTCAGGNC	CNNNGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANN	G			751

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTCAGA	ACTCANTGCC	AAGANCCCTG	AAACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCATTTT	GCTCATCTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCAACAT	GGCTGAGCAC	TTCCGTACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTTT	600
GAAGANTCAC	CTACTTCAAA	GAAAANAGTG	CCTTTCCCCC	ATTTCCTGTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGTCC	CCAACCANA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCCA	TAACAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTCGCTGA	AGGGGTTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTCCC	TTTGTCACTG	GGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAAC	GGTGGGCTGA	300

CANGTGCCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGCACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGGG	TCNTANTACC	ANC GTGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGTT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCCTCNTGG	GTTGNNCTTG	AACCTAATCN	CCNNTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTNTTC	780
CACAACCCTN	CCCCACCCAC	GGGTTCNGNT	GGTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAAACCCCTG	GTGCTGAAGG	60
ATGTGGAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGACTAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGTG	420
TGCAAGGTGG	GCCTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCC	CAGGGCCCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTAAAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCC GG	660
CNCCTCCNTT	TTCCCCNNNT	AACAAAGGGC	NCTNGCNTTT	GAACTGCCCN	AAACCCNGAA	720
TCTNCCNNNG	AAAAANTNCC	CCCCCTGGTT	CCTNNANCC	CCTCCNCNA	ANCTNCCCCC	780
CCC						783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCAC	GTTCTCTTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCA	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCAGGGCA	420
CACTTGTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAA	GACCACAAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540

TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACTGC	600
CNACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACTGAAA	CCNTGCATGG	TGCCCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CACTGCCATG	CAGTTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCGGGCG	TTGTGGCTT	TGCTCTTGGT	TTCCCTGGGCT	GCTATGGTGC	360
TAAGACGGAG	AGCAAGTGTG	CCCTCGTAC	GTTCTTCTTC	ATCCTCTTCC	TCATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	TGGTCGCCCT	GGTGTACACC	ACAATGGCTG	AACCATTCCCT	480
GACGTTGCTG	GTANTGCCCTG	CCATCAANAA	AGATTATGGG	TTCCCAGGAA	AAATTCACTC	540
AANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTCTGN	TGGCTTCCCC	AACTATAACCG	600
GAATTGAA	AGANTCNCCC	TACTTCCAAA	AAAAAANANT	TGCCTTNCC	CCCNNTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAATN	AAAACCTGCC	CNNNCAAAAA	GGNTCNAAA	720
CAAAAAAANT	NNAAGGGTTN					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGCCAC	GAAGCACGTC	AGCATAACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATACACTT	TACTTTAGCA	GCCAGGGTGA	CAACTGAGAG	GTGTGAGAGC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCAT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACA	CGTAGACACC	AGNGGCCTCC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTGG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCC	TGTCACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGACG	TGGTTCCGCC	CCCTCNCTTA	ATGACACCAG	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTGTCAG	CTGGGTTCAGG	GTCTGCTGGC	CNCTACTTGC	600
AANCCTCGTC	NGGCCCATGG	AATTACCCNC	ACCGGAACCTN	GTANGATCCA	CTNNTCTAT	660
AACCGGNCGC	CACCGCENNNT	GGAACCTCCAC	TCTTNTTNCC	TTTACTTGAG	GGTTAAGGTC	720
ACCCCTNNCG	TTACCTTGGT	CCAAACCN	CCNTGTGTCG	ANATNGTNAA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACGNGGNG	GNGTCTTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGAGTG	CAGAACTGAA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANN	TGCTCCNNTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCENNNGA	300
CATGCCCGAGN	GTTANATAAC	NGGCNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACCTGACTA	CTTAACTGAA	CCCNNGAATC	TNCCNCCCCCT	420
CCACTAAAGCT	CAGAACAAAA	AACCTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTACCC	CATNCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTCTG	ACTGCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCCAAT	CCCCCCAACC	NTNAATTNAN	TTTANCCCN	660
CCCCCNNGCC	CGGCCTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNNGC	TTTNCCCAAC	720
NNAATCCNCC	T					731

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCCCTC	NTCCAATNN	CCNTTCCGG	GNGGGGTTC	CAAACCCAAN	TTANNTTG	120
ANNTTAAATT	AAATNTNNT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCTGAAA	CCNGTNGNTT	CCAAAAATNT	TTAACCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTTCTCN	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTNGCCAC	GCTGAAATTA	ATTGGNTTCC	GNTGTTTCC	NTTAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTACGG	GGNNNNNTCCC	TNTTGGGGGG	CNGGNNC	CCCCNTCGGG	480
GGTTNGGGNC	AGGNCNAAT	TGTTTAAGGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTTT	NCCCCCCCCC	CANGCCCC	CTCGNANAGT	TGGGGTTGG	600
GGGGCCTGGG	ATTTTNTTTC	CCCTNTTNC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCN	GGCCCCNCCN	AAGANTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGC	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCNC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNNTN	NATCACNCNC	CNCCNACTAC	GCCCNCNANC	CNACGCNCTA	120
NNCANATNCC	ACTGANNGCG	CGANGTNGAN	NGAGAAANCT	NATACCAAG	NCACCCANACN	180
CCAGCTGTCC	NANAANGCCT	NNNATACNGG	NNNATCCAAT	NTGNANCCTC	CNAAGTATTN	240
NNCNCCNAT	GATTTTCCTN	ANCCGATTAC	CCNTNCCCC	TANCCCTCC	CCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNGCNCNCC	CCGCTAGNTC	CCCNNAAGT	CNCNCNCTA	360
AACTCANCCN	NATTACNCGC	TTCNTGAGTA	TCACTCCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATAACAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	CTAATACTTC	CAGTCTNCCT	TCNCCAATT	CCNAANGGCT	540
CTTCNGACA	GCATNTTTG	GTTCCCNNTT	GGGTTCTTAN	NGAATTGCC	TTCNTNGAAC	600
GGGCTCNTCT	TTTCCTTCGG	TTANCCTGGN	TTCNNCCGGC	CAGTTATTAT	TTCCCNNTTT	660
AAATTCTNC	CNTTANTTT	TGGCNTTCNA	AAACCCCGGC	CTTGAAAACG	GCCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTGTTTT	GTTCC			755

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGGCCNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTCCN	NCCCCNNCNG	ACCCNGGCGA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCCTCCANT	NNGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCN	GGGTNCTTCG	GTTGTCGANT	CNACCGNANG	CCANGGATT	CNAAGGAAGG	480
TGCGTTNTTG	GCCCTTACCC	TTCGCTNCGG	NNCACCCCTC	CCGACNANGA	NCCGCTCCCG	540
CNCNNCGNNG	CCTCNCTCG	CAACACCCGC	NCTCNCTNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNNGACNN	NAGCNCNNTC	GCNCGGCGCN	GCGNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNA	CNAAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCCGN	CTTCCNACCC	ANGNNNTCCN	CGAGGACACN	NNACCCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAAC	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCCTC	CGCAACCATG	60	
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120	
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNG	AGAACCAANG	180	
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GT	TTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTGGGA	300	
TCGGGTTTNN	NNTGACCGNG	CNNCCCCCTC	CCCCNTCCAT	NACGANCCNC	CCGCACCAACC	360	
NANNGCNGC	NCCCCGNNCT	CTTCGCCNCC	CTGTCTNTN	CCCCTGTNGC	CTGGCNCNGN	420	
ACCGCATTGA	CCCTCGCCN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCCTG	480	
TGGGNNNNGCG	TCTGCNCCGC	GTTCCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540	
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCCTT	600	
CGNCGTGNCC	CGNCCCCACC	NTCATTTNCA	NACGNTCTTC	ACAANNNCT	GGNTNNCTCC	660	
CNANCNGNCN	GTCANCCNAG	GGAAAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGN GANGTC	720	
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780	
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840	
TNACCNNTAC	GANTNTCGN	CNCCCTCTTT	CC			872	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATT	TATAGNGTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTC	CAAAT GTATA	CNAAN TANAT	TATGAA	TCTNATNTGA	120
TCNTNCATTA	GTAACA	ANTG TNNTGTC	CAT	CCAT	TCNACN	180
CGCATT	CNCANTATN	TAATNGGGAA	NTCNNTNNN	NCACCN	NCAT CTATC	240
GCNC	CTGAC	TGGNAGAGAT	GGATNANTTC	TNNTNTGACC	NACATGTTCA	300
GCNC	CCCTGAC	TGGNAGAGAT	GGATNANTTC	TNNTNTGACC	NACATGTTCA	360
AANAN	CCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	420
AACCT	TGCGTC	AGANN	CATCA AACNTGGAA	ACCCG	CCNCC ANGTTNAAGT	480
GATCCC	GTGTC	AGGNT	TTNACC ATCC	CTTCNC	AGCGCCCCCT	540
GTGTCC	NANC	CNCT	CAACAT GANAC	CGC	AGNCCANCCG CAATTNGGCA	600
GAAC	CCCCCTA	GGGG	GANTNA TNCAA	ANCCC	CAATGTCNC CAGGATTGTC	660
CCC	CCCTTGG	GGG	GACNGTGACC	AANT	CCCGGA GTNCCAGTCC	720
CCC	ACCGGT	GGG	GGGTGAANCT	CNGN	NTCNGAGGN NTCGNAAGGA	780
ACCG	NCNTGGG	GGG	CANCNTCNGA	AGNGCC	NCNT CGTATAACCC CCCCTCNCCA	840
NCCNACNGNT	AGNT	CCCCCCC	CNGGGTNC	GGG	AAANGG	872

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCACG TCATCCAGCA GAGAATGGAA	120
AGTCAAATTI CCTGAATTGC TATGTGTCTG GGTTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTC AGACTTGTCT TTCAGCAAGG	240
ACTGGTCTTT CTATCTCNTG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCATGTG ACTTTGTAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTGTAAAGAT GCGCATTG GATTGGATGA ATTCAAATT	420
CTGCTTGCTT GCNTTTAAT ANTGATATGC NTATACACCC TACCCCTTAT GNCCCCAAT	480
TGTAGGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCNTTCG	540
AATTGCCGT CNCCNGTTN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTNCC	600
TCTTACGGAA GGGCCTGGGC CNCTTNCAA GGTTGGGGA ACCNAAAATT TCNCTNTGC	660
CCNCCCNCCA CNNTCTGNG NNCNCANTTT GGAACCTTC CNATTCCCCT TGGCCTCNNA	720
NCCTNNCTA ANAAAACCTN AAANGTNGC NAAANNTTN ACTTCCCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTAAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTTCTGCA	120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCCAGAG GGGTGGTAG	180
CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAAACAN ACCACAGAGC ANACAGACCA	240
NTGATGACCA TGGGGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCTTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCTG GGANCAGCTA	420
ACNAGCACT CACCTGCCCT CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT	480
CCCTGTTGGA ATTNCGGGA NACCAAGGGA NCCCCCTCCT CCANCTGTGA AGGAAAANN	540
GATGGAATTN TNCCCTTCCG GCCNNTCCCC TCTTCCTTTA CACGCCCTT NNTACTCN	600
TCCCTCTNTT NTCCCTGNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TCGGANNCTN	660
GANATTCCAC TNNGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT	720
GGNNNCCTCG NTCATCCTCT CTTTTTCNCT ACCNCCNNTT CTTTGCTCT CCTTNGATCA	780
TCCAACCNTC GNTGGCCNTN CCCCCCNNN TCCTTNCCCC	820

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT GGCCTCTTCC TCCTCAGGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT	60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTCAAGCCCT GCCAACCTG ATTCTGATGA	120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGCGC	180
CTGCTGAGCA CTTCCGCCCT TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGTC	240
TCCGCCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC	300

TTCTTCCTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNA	ACCGNGCTTNC	CNTCNTCTCC	CCNTANCCCG	CCNGGGAANC	540
CTCCTTGCCT	CTNACCANGG	GCCNNNACCG	CCCNTNNCTN	GGGGGGCNNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCNNT	TNCCTCGTCC	CNNCNNGCN	NNGCANNTTC	NCNGTCCCNN	660
TNNCTCTCN	NGTNTCGNAA	NGNTCNCNTN	TNNNNNGNCN	NGNTNNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNTTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNTNNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNCTC	CCGGCCNC			818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGGTGTG	60
TCCAACATG	ANGGTGNNGT	TCTCTTTGA	ANGAGGGTTG	NGTTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNNAAAAGGN	TTTNAGGGAT	TTTCGGCTC	TTATCAGTAT	180
NTANATTCCCT	GTNAATCGGA	AAATNATNTT	TCNNCNGAA	AATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCT	TCGCCCTNTG	ACTCTGCNNG	AGCCAATAC	CCNNNGNAT	GTCNCCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNN	480
CGTTTCNCAT	NAAGGCACCTT	TNGCCTCATC	CAACCNCTNG	CCCTCNCCCA	TTTNGCCGTC	540
NGGTTCNCCCT	ACGCTNNNTNG	CNCCTNNNTN	GANATTTCNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGTA	GGGNCTTNTC	TTTNACCN	GNGGTNTACT	AATCNCTNC	ACGCNTNCTT	660
TCTCNACCCC	CCCCCTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGG	720
NNNCCANNC	C					731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNN	120
ATNTNTACNC	TCATANNCCCT	CNNNACCCAC	TCCCTCTTAA	CCCNACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAACNC	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTCNC	ATNANCTCCT	AATTGAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TTCNCCAACC	NTTNCCCTCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCG	GCAAGCCNAN	GGNCATTTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCNNAT	CTCCCTAANA	600

AATNCTCCTN NAATTACTN NCANTNCCAT CAANCCCACN TGAAACNNAA CCCCTGTTT	660
TANATCCCTT CTTTCGAAAA CCNACCCTT ANNNCCAAC CTTTNGGGCC CCCCCNCTNC	720
CCNAATGAAG GNCNCCAAT CNANGAAACG NCCNTGAAAA ANCNAAGGCNA ANANNNTCCG	780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCCNGGCC CC	822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG CTCTGGCACA TGCCTCCTGA ATGGCATCAA AAGTGATGGA CTGCCATTG	60
CTAGAGAAGA CCTTCTCTCC TACTGTCTT ATGGAGCCCT GCAGACTGAG GGCTCCCTT	120
GTCTGCAGGA TTTGATGTCT GAAGTCGTGG AGTGTGGCTT GGAGCTCCTC ATCTACATNA	180
GCTGGAAGCC CTGGAGGGCC TCTCTCGCCA GCCTCCCCCT TCTCTCCACG CTCTCCANGG	240
ACACCAGGGG CTCCAGGCAG CCCATTATTC CCAGNANGAC ATGGTGTTC TCCACGCGGA	300
CCCATGGGGC CTGNAAGGCC AGGGTCTCTT TTGACACCAT CTCTCCCGTC CTGCCTGGCA	360
GGCCGTGGGA TCCACTANTT CTANAACGGN CGCCACCNCG GTGGGAGCTC CAGCTTTGT	420
TCCCNTTAAT GAAGGTTAAT TGCGCGCTT GCGTAATCAT NGGTCANAAC TNTTCCCTGT	480
GTGAAATTGT TTNTCCCTC NCNATTCCNC NCNACATACN AACCCGGAAN CATAAAGTGT	540
TAAAGCCTGG GGGTNGCTN NNGAATNAAC TNAACTCAAT TAATTGCGTT GGCTCATGGC	600
CCGCTTCCN TTCNGGAAA CTGTCNTCCC CTGCNTTNNT GAATCGGCCA CCCCCCNGGG	660
AAAAGCGGTT TGCNTTTNG GGGGNTCCTT CCNCTCCCC CCTCNCTAAN CCCTNCGCCT	720
CGGTGTTNC NGGTNGCGGG GAANGGGNAT NNNCTCCCNC NAAGGGGGNG AGNNNGNTAT	780
CCCCAAA	787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT TTTTTTTGGC GATGCTACTG TTTAATTGCA GGAGGTGGGG GTGTGTGTAC	60
CATGTACCAAG GGCTATTAGA AGCAAGAAGG AAGGAGGGAG GGCAGAGCGC CCTGCTGAGC	120
AACAAAGGAC TCCTGCAGCC TTCTCTGTCT GTCTCTTGGC GCAGGCACAT GGGGAGGCCT	180
CCCGCAGGGT GGGGGCCACC AGTCCAGGGG TGGGAGCACT ACANGGGGTG GGAGTGGGTG	240
GTGGCTGGTN CNAATGCCCT GNACACANATC CCTACGATT TTGACACCTG GATTCACCA	300
GGGGACCTTC TGTTCTCCA NGGNAACTTC NTNNATCTN AAAGAACACA ACTGTTCTT	360
CNGCANTTCT GGCTGTTCAT GGAAGCACA GGTGTCNNAT TTNGGCTGGG ACTTGGTACA	420
TATGGTTCCG GCCCACCTCT CCCNTCNAAN AAGTAATTCA CCCCCCCCCC CCNTCTNTTG	480
CCTGGGCCCT TAANTACCA CACCGGAAC TANTTANTTA TTCATCTTNG GNTGGGCTTG	540
NTNATCNCCN CCTGAANGCG CCAAGTTGAA AGGCCACGCC GTNCCCNCTC CCCATAGNAN	600
NTTTTNNCNT CANCTAATGC CCCCCCNNGC AACNATCCAA TCCCCCCCCC TGGGGGCC	660
AGCCCANGC CCCCCNCTCG GGNNNCCNGN CNCGNANTCC CCAGGNTCTC CCANTCNGNC	720
CCNNNGCNCC CCCGCACGCA GAACANAAGG NTNGAGCCNC CGCANNNNNN NGGTNNCNAC	780
CTCGCCCCCCC CCNNCGNNG	799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNTCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTN	AATTTCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACATTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTG	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCTGGCC	CCCAAATCCT	CCCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCNNNCA	CCATCCCCCC	NNGNNAACGNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCAATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTGTC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTTC	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNNGCCACCC	CCCGGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTCGG	CTTGCAGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGG	ACCGTAAAG	CCCCAATCTT	60
ANCAAGTGC	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCTG	CTGTCCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANC GGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCTTGG	GCAAACTGTA	TGGANGGCAG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCC GCCATC	CGGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAA	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAACAN	CAGGATNTGA	GTCTTGATT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGC NCAAAATC	CGACTCCCCN	TCCCTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCN TCCNN	CAGGGTTGGT	GGCANNCCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCNT	660
ACNTNCTGGG	CCGGGTTC	AA ANTCCCTCCN	TTGNCNNTC	CCTCGGGCCA	TTCTGGATT	720
NCCNAACTTT	TTCCCTTCCC	CNCCCCNCGG	NGTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTCCCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCN	TNG GGCC	834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTCCA	TGACNAAGGC	TCCCCTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCCGTGA	180
GGAAAGGCCT	GCCTTGTAAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGTGG	TATCACTGCC	ACNTTCCAC	CCAGCTGGC	NCCCTTCCCC	CATNTTGTG	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNNCAGTG	GATCTGCCAA	ANANTACCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCCCT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAG	GAATGTTCT	GGGTCCANT	CCCTCCTTIG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGT	CGCTGAAGGG	GTTGTAGTAC	CAGCGGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTCGATN	CANCAGCCC	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCCTNANCC	CAAAC TGCC	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCACTNNN	TACCANGGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTGAAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCCTCTNCC	CTAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTAAAAAA CCCCTCCAT TGAATGAAAA

60

CTTCCNAAAT	TGTCCAACCC	CCTCNNCAA	ATNNCCATT	CGGGGGGGGG	GTTCCAAACC	120
CAAATTAATT	TTGGANTTTA	AATTAATNT	TNATTNGGG	AANAANCAA	ATGTNAAGAA	180
AATTTAACCC	ATTATNAACT	AAATNCCTN	GAAACCCNTG	GNTTCCAAA	ATTTTAACC	240
CTTAAATCCC	TCCGAAATTG	NTAANGAAA	ACAAATTTCN	CCTAAGGCTN	TTTGAAGGTT	300
NGATTAAAC	CCCCTTNANT	TNTTTTNACC	CNNGNCTNAA	NTATTTNGNT	TCCGGTGT	360
TCCTNTTAAN	CNTNGGTAAAC	TCCCNGTAAT	GAANNNCCT	AANCCAATTA	AACCGAATT	420
TTTTTGATT	GGAAATTCCN	NGGAAATTNA	CGGGGGTTT	TCCCNTTTGG	GGGCCATNCC	480
CCCNCTTTCG	GGGTTGGGN	NTAGGTTGAA	TTTTTNANG	NCCCCAAAAA	NCCCCAANA	540
AAAAAACTCC	CAAGNNTTAA	TTNGAATNTC	CCCCTTCCCA	GGCCTTTGG	GAAAGGNGGG	600
TTTNTGGGGG	CCNGGGANTT	CNTTCCCCCN	TTNCCNCCCC	CCCCCCNGGT	AAANGTTAT	660
NGNNTTGGT	TTTGGGCC	CTTNANGGAC	CTTCCGGATN	GAAATTAAAT	CCCCGGGNCG	720
					GCCG	724

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT	TTTTTCTTTG	CTCACATT	ATTTTATTT	TGATTTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTTCAT	TTGTTTCTTT	TATTTCATTT	TATTTGTTTG	CTGCTGCTGT	120
TTTATTATT	TTTACTGAAA	GTGAGAGGG	ACTTTGTGG	CCTTTTTTC	TTTTCTGTA	180
GGCCGCCTTA	AGCTTTCTAA	ATTGGAACA	TCTAACAG	CTGAANGGAA	AAGGGGGTTT	240
CGAAAATCA	CTCGGGGAA	NGGAAAGGTT	GCTTTGTTAA	TCATGCCCTA	TGGTGGGTGA	300
TTAACTGCTT	GTACAATTAC	NTTCACTTT	TAATTAATTG	TGCTNAANGC	TTAAATTANA	360
CTTGGGGGTT	CCCTCCCCAN	ACCAACCCCN	CTGACAAAAA	GTGCCNGCCC	TCAAATNATG	420
TCCCCGCNT	CNTGAAACA	CACNGCNGAA	NGTTCTCATT	NTCCCCNCNC	CAGGTAAAAA	480
TGAAGGGTTA	CCATNTTAA	CNCCACCTCC	ACNTGGCENN	GCTCTGAATCC	TCNAAAANCN	540
CCCTCAANCN	AATTNCTING	CCCCGGTCNC	GCNTNNGTCC	CNCCCGGGCT	CCGGGAANTN	600
CACCCCNNGA	ANNCNNTNNC	NAACNAAATT	CCGAAAATAT	TCCCNNTCNC	TCAATTCCCC	660
CNNAGACTNT	CCTCNANCAN	CNCAATTTC	TTTNNTCAC	GAACNCGNNC	CNNAAAATGN	720
NNNNCNCC	CNCTNGTCCN	NAATCNCCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATT	CTGTAAGATC	AGGTGTTCC	CCCTCGTAGG	TTTAGAGGAA	ACACCCCTCAT	60
AGATGAAAC	CCCCCCGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGG	GTAGGAGGG	120
CGCCCTATGC	ACAGCTGGC	CCTTGAGACA	GCAGGGCTTC	GATGTCAGGC	TCGATGTCAA	180
TGGCTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAAC	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTGGGGT	300
CGGTCTATAAN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCCGCA	CCGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGCT	420

CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCNGN	ATGCCAANCA	NCCCCAANCC	CCGGGGTCCT	540
AAANCACCCN	CCTCCTCNNT	TCATCTGGGT	TNTTNTCCCC	GGACCNTGGT	TCCTCTCAAG	600
GGANCCCATA	TCTCNACCAN	TACTCACCN	NCCCCCCCNT	GNNACCCANC	CTTCTANNGN	660
TTCCCNCNN	NCCTCTGGCC	CNTCAAANAN	GCTTNACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCCTATCT	GNACCCNCN	TTTGTCTCAN	TNT			753

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATTT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTCCAC	120
TTCTTTAAC	CTTGTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTCAGAG	GTATTTCAT	300
TTTACTTTT	TGATTAATTG	TGTTTTATAT	ATTAGGGTAG	T		341

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTTCAAACA	TTCTAAATAA	ATAATTTCA	GTGGCTTCAT	A		101

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo spiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAGTAAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTGAA AATATTACG TCCAGGAGTT CTTTGTTTCT	60
GATTATTTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT	120
CTCTCCATCC TCGGGCATTTC TTCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTCAATGC	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTITA TTAATCCTGG GTTCTTGTCT GGGTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTAUTGC	660
ACTGGCCGTT CCACCTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACATCATGC TGCAAAAGGTG CTCGCCGTTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
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AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGT CTGCTGGCGA ACGGCAGAAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATATTCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTA	240
AAAGCTTCAGT AAANAAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGTCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAG GACACATGCT	540
GCCTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAAACAGAAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AACATCAAAG AAAGGAAGGT GGCAGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCTTG CTCCCTGCAG CCTGTAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCCTG ATTACTCCAG CATCTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGCTCATTAC ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACCTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTCCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCA CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTTAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACTTCTT GTATCAATT TTGTTGTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTCANA TGGTAGCTTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420
CAATTATTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAT CCAAGTTAAT	480
ATCACTCTG T	491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTAA TATGCAGCAT TTTCTTTTG CTTTGATAAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAA GTTCAGAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTTGAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTT GGAACAGAAA GGGAAAANC	300
AGCTTGANT TTCTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTG GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCACAAA CATATTCCAA CTCAACACTT CTTTCCNCG	420
TANCTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NC GGATGTT	480
CANT	484

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTGTTTG T	151

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTCTTAT GTAAGGGACT TGAGTATACT 60
 TGGATTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC 120
 AAGGGACAAC TGT 133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA	ACCTGAGCCG	CTGCTCCGCC	TCTGGGATGA	GGTGATGCAN	GCNGTGGCGC	60
GACTGGGAGC	TGAGCCCTTC	CCTTTGCGCC	TGCCTCAGAG	GATTGTTGCC	GACNTGCANA	120
TCTCANTGGG	CTGGATNCAT	GCAGGGT				147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT	AGGTTTNAAG	TTATTGTNAT	TGTAAAATAC	ATTGAATTTC	CTGTATACTC	60
TGATTACATA	CATTTATCCT	TTAAAAAAAGA	TGTAAATCTT	AATTTTATG	CCATCTATTA	120
ATTTACCAAT	GAGTTACCTT	GTAAATGAGA	AGTCATGATA	GCACGTGAATT	TTAACTAGTT	180
TTGACTTCTA	AGTTTGTT					198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTC	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCCTCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA

30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTTATAT TTAATGCTTC
CTGTATGAAT AAAAATGGTT ATGTCAAGT

60

89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT

60

97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAAACAANAA	NTCCCTTCTT	TAGGCCACTG	ATGGAAACCT	GGAACCCCCT	TTTGATGGCA	60
GCATGGCGTC	CTAGGCCTTG	ACACAGCGC	TGGGGTTTGG	GCTNTCCCAA	ACCGCACACC	120
CCAACCCTGG	TCTACCCACA	NTTCTGGCTA	TGGGCTGTCT	CTGCCACTGA	ACATCAGGGT	180
TCGGTCATAA	NATGAAATCC	CAANGGGAC	AGAGGTCAGT	AGAGGAAGCT	CAATGAGAAA	240
GGTGCTGTTT	GCTCAGCCAG	AAAACAGCTG	CCTGGCATTC	GCCGCTGAAC	TATGAACCCG	300
TGGGGGTGAA	CTACCCCCAN	GAGGAATCAT	GCCTGGCGA	TGCAANGGTG	CCAACAGGAG	360
GGCGGGAGG	AGCATGT					377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC	CTCAGAATT	AGGAAAGAGA	CTGTCGCCTG	CCTTCCTCCG	TTGTTGCGTG	60
AGAACCCGTG	TGCCCCTTCC	CACCATATCC	ACCCTCGCTC	CATCTTGAA	CTCAAACACG	120
AGGAACTAAC	TGCACCCCTGG	TCCCTCTCCCC	AGTCCCCAGT	TCACCCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGGTTT	240
TTATATATTT	TTTAATAAGA	TGCACTTTAT	GTCATTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTAAA	AAAGGGACT	TGCTTAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TG TGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCCAG	GGCCCCAGCC	TGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTCT	GTGCTAGTGG	ACCGT				385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGAA TTCCATTGTG TTGGGGCTC TCACCCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCC CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CGGTTGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAACTGCAG AAGAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCCT GGGGAGAACAA	480
GAANGTCCCT GGGTGAATC CAGGTGTCAA GAAATCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACCTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAACAGGAGAACAGCACATACCAA GGCCACCA CACCACCTGT	180

CCAAAAGGC	CTTCGATACG	GGATAATCCT	ATTTATTACC	TCAGAAGTTT	TTTCTTCGC	240
AGGGATTTT	CTGAGCCTTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGGCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCTAGA	AGTCCCACTC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TAATGGGTCT	CTATT	477

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTCTACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGTAA	AGAAAGAAAT	CACACCATTA	ATAATGGTAA	GATTGGTTA	120
TGTGATTTA	GTGGTATTTT	TGGCACCCCTT	ATATATGTTT	TCCAAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACCTAAAA	AGTGAGTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTTGTCTACT	TTAAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTTG	CCTTGAAAAAA	TATCAAATAT	AACTCTTAGA	GAAATGTACA	TAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATT	TATTTTAAA	AAGTACATGG	480
TAAAAAAAAA	AATTACAAC	AGTATATAAG	GCTGTAAAAT	GAAGAATTCT	GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAAGAACAC	AAAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTGGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGGTTTGAAA	ACCGTTCTNC	AAATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCCC	GTCTGTTATG	420
ATTTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNGGAGG	A			511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	TTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	GTAACTCTG	CCAGTCTTC	TCTTCAGGCC	AGGGTGCATC	240
CTCAGAACCC	TACTAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	300
CTCTGCATTA	AATCTATTG	CCATTTCTGA	AAAAAAAAAA	AAAAAAAGGG	CGGCCGCTCG	360
ANTCTAGAGG	GCCCCTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCTTCT	ANTTGCAGC	420
CATCTGTTGT	TTGCCCTCCTC	CCCGNTGCCT	TCCTTGACCC	TGGAAAGTGC	CACTCCCACT	480
GTCCTTCCT	AANTAAAAT					499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATT	GGATTCAAGCC	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAGAGCTA	GTCTCTAACT	120
TCCAGGCCCA	CGGCTCAAGT	GAATTGAAAT	ACTGCATT	CAGTGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGT	TCTTACCACT	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGT	TGATTGAATT	CTAAAAATGG	TAATCATTAG	300
GGCTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTTGCTT	GATATATTG	TTGATATTAA	GATTCTGAC	TTATATTG	AATGGTTCT	420
ACTGAAAAN	GAATGATATA	TTCTTGAAGA	CATCGATATA	CATTATTTA	CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCC	CAAATTGTAT	GGTGATAAAA	GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATTTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAAGG	AGGCCATCTT	TTCCATCG	GTTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTCT	GGGTTTGGGC	CATTTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAACAA	TCCCTGN		467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCAAA	GATTCAAGGT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTTC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAAGTG	GAGCATTAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGCTTTCT	ATCTCTTGT	CTACACTGAA	TTCACCCCCA	300
CTGAAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTITC	AAGCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CGGCGGGGGA	TGCGAGGCTC	GGAGCACCCT	TGCCCGGCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTTCTGTCC	CTTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTCATATCT	GGAGCCTGAT	GTCTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAA						248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTGC CGCGCCCAA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTCT ATAAATGCCT	180
GATTTAAAAA AAAAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTGTT AGGTTTTGGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT	120
CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCCCTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTAA	420
TTCCCAGGAA TATGGGGTTC ATTATATGAAT ANTACCCGGG ANAGAAGTT TGANTNAAAC	480
CNGTTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT	GAGATGCTAA	GGCCCAGAG	ATCGTTGAT	CCAACCCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCTGGCCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGT	180
GCAATTACAG	TTGCCACCTC	CAACTTAAAC	ATTCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTTAAACT	TTCCCACCCA	GAAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTCATAC	300
TCTTCTAAGT	CCTCTCCAG	CCTCACTTTG	AGTCCTCCTT	GGGGGTTGAT	AGGAANTNTC	360
TCTTGGCTTT	CTCAATAAAA	TCTCTATCCA	TCTCATGTTT	AATTGGTAC	GCNTAAAAAT	420
GCTGAAAAAA	TTAAAATGTT	CTGGTTTCNC	TTTAAAAAAA	AAAAAAAAAA	AAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG	TATGCCNTCN	CTGTGGNGTT	ATTGTTGCTG	CCACCCCTGGA	GGAGCCCAGT	60
TTCTCTGTA	TCTTTCTTTT	CTGGGGGATC	TTCCTGGCTC	TGCCCTCTCCA	TTCCCAGCCT	120
CTCATCCCCA	TCTTGCACCT	TTGCTAGGGT	TGGAGGCGCT	TTCCCTGGTAG	CCCCTCAGAG	180
ACTCAGTCAG	CGGGAATAAG	TCCTAGGGT	GGGGGGTGTG	GCAAGCCGGC	CT	232

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC	AGAACGCTAAA	GCCAAAGCCC	AAGAACGAGTG	GCAGTGCCAG	CACTGGTGC	60
AGTACCAAGTA	CCAATAACAT	GCCAGTGCCA	GTGCCAGCAC	CAGTGGTGGC	TTCAGTGCTG	120
GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	TGGCCTTGGT	GGAGCTGGTG	180
CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	CAAGTGAGAT	TTTAGATATT	240
GTAAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	CTCAGAAACC	TACTCAACAC	300
AGCACTCTNG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	CTCTGCATTA	AATCTATTG	360
CCATTCAAA	AAAAAA	AAA				383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTCCTC	CAGTATTACC	TCAACGAGCA	60
GGGAGATCGA	GTCTATACGC	TGAAGAAATT	TGACCCGATG	GGACAACAGA	CCTGCTCAGC	120
CCATCCTGCT	CGGTTCTCCC	CAGATGACAA	ATACTCTCGA	CACCGAATCA	CCATCAAGAA	180
ACGCTTCAAG	GTGCTCATGA	CCCAGCAACC	GCGCCCTGTC	CTCTGAGGGT	CCTTAAACTG	240
ATGTCTTTTC	TGCCACCTGT	TACCCCTCGG	AGACTCCGTA	ACCAAACCTCT	TCGGACTGTG	300
AGCCCTGATG	CCTTTTGCC	AGCCATACTC	TTTGGCNTCC	AGTCTCTCGT	GGCGATTGAT	360
TATGCTTGTG	TGAGGCAATC	ATGGTGGCAT	CACCCATNAA	GGGAACACAT	TTGANTTTTT	420
TTTCNCATAT	TTTAAATTAC	NACCAGAATA	NTTCAGAATA	AATGAATTGA	AAAACCTCTTA	480
AAAAA	AAAA					494

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC	TATGGCGTGG	CCACGGANGG	GCTCCTGAGG	CACGGGACAG	TGACTTCCCA	60
AGTATCCTGC	GCCGCGTCTT	CTACCGTCCC	TACCTGCAGA	TCTTCGGGCA	GATTCCCCAG	120
GAGGACATGG	ACGTGGCCCT	CATGGAGCAC	AGCAACTGCT	CGTCGGAGCC	CGGCTTCTGG	180
GCACACCCCTC	CTGGGGCCCA	GGCGGGCACC	TGCGTCTCCC	AGTATGCCAA	CTGGCTGGTG	240
GTGCTGCTCC	TCGTCATCTT	CCTGCTCGTG	GCCAACATCC	TGCTGGTCAC	TTGCTCATTG	300
CCATGTTCAAG	TTACACATTC	GGCAAAGTAC	AGGGCAACAG	CNATCTCTAC	TGGGAAGGCC	360
AGCGTTNCCG	CCTCATCCGG					380

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CCTCCTGCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CCGTCNATNA	AACCTGTGGC	TGGTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAACG	GAGTGCCTGA	TCTTCCCCAC	ACTTTTGATG	ACTTTATTGA	240
GTGAGATTCTG	CATGTCAGC	AGGAGGTTGT	ACCAGCTCTC	TGACAGTGAG	GTCACCAAGGCC	300
CTATCATGCC	NTTGAACGTG	CCGAAGAACAA	CCGAGCCTTG	TGTGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAAGA	NAGCCGTGGC	AAAAGANATT	GACAACCTCGC	CCAGGNNNGAA	420
AAAGAACACC	TCCTGGAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNNGC	GCNTNCCTTT	480
T						481

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGCTG	AGAATTCAATT	60
ACTTGGAAAA	GCAACTTNAA	GCCTGGACAC	TGGTATTAAGA	ATTCAACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTGC	TCCCTTACTT	TGTCATCAC	AGTCTGGAA	TAAGGGTATG	180
CCCTATTACAC	ACCTGTTAAA	AGGGCGCTAA	GCATTTTGAA	TTCAACATCT	TTTTTTTTGA	240
CACAAGTCAG	AAAAAAGCAA	AAGTAAACAG	TTNTTAATTT	GTAGCCAAT	TCACTTTCTT	300
CATGGGACAG	AGCCATTGAA	TTTAAAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAGANTAG	CCTTCTACT	TCACCAGACA	CAACTCCTTT	CATATTGGGA	420
TGTTNACNAA	AGTTATGTCT	CTTACAGATG	GGATGCTTTT	GTGGCAATTG	TG	472

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTTGACTAGG	300
GGGGACAAAG	AAAAGCANAA	CTGAACATNA	GAAACAATTN	CCTGGTGAGA	AATTNCATAAA	360
ACAGAAATTG	GGTNGTATAT	TGAAANANNG	CATCATTNA	ACGTTTTTT	TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT	CCTCTCTATC	TAGCTCCAGC	CTCTCGCCTG	CCCCACTCCC	CGCGTCCC	60
GTCCTAGCCN	ACCATGCCG	GGCCCGCTCG	CGCCCCGCTG	CTCCTGCTGG	CCATCCTGGC	120
CGTGGCCCTG	GCGTGAGCC	CCGCGGCCGG	CTCCAGTCCC	GGCAAGCCGC	CGCGCCTGGT	180
GGGAGGCCCA	TGGACCCC	GTGGAAGAAG	AAGGTGTGCG	GCGTGCACTG	GACTTTGCCG	240
TCGGCNANTA	CAACAAACCC	GCAACNACTT	TTACCNAGCN	CGCGCTGCAG	GTTGTGCCG	300
CCCAANCAA	TTGTTACTNG	GGGTAANTAA	TTCTTGGAAAG	TTGAACCTGG	GCCAAACNNG	360
TTTACCAAGAA	CCNAGCCAAT	TNGAACATT	NCCCCCTCCAT	AACAGCCCC	TTTAAAAAGG	420
GAANCANTCC	TGNTCTTTTC	CAAATTT				448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG	CACTGGCAC	TGTGATGGAA	CCATTGGGCC	AGGATGCTTT	GAGTTATCA	60
GTAGTGATT	TGCCAAAGTT	GGTGTGTAA	CATGAGTATG	TAAAATGTCA	AAAAATTAGC	120
AGAGGTCTAG	GTCTGCATAT	CAGCAGACAG	TTTGTCCGTG	TATTTTGTTAG	CCTTGAAAGTT	180
CTCAGTGACA	AGTTNNTTCT	GATGCGAAGT	TCTNATTCCA	GTGTTTTAGT	CCTTGCATC	240
TTTNATGTTN	AGACTTGCCT	CTNTNAAATT	GCTTTTGTNT	TCTGCAGGTA	CTATCTGTGG	300
TTTAACAAAA	TAGAANNACT	TCTCTGCTTN	GAANATTGAA	ATATCTTACA	TCTNAAAATN	360
AATTCTCTCC	CCATANNAAA	ACCCANGCCC	TTGGGANAAT	TTGAAAAAANG	GNTCCTTCNN	420
AATTCNNANA	ANTTCAGNTN	TCATACAACA	NAACNGGANC	CCC		463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCTGAA	GCNTNTTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTGTAA	AGACTTCATC	TGGTAAAGTC	TTAACGTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCTTGAAGT	ATTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTAAATA	TACTTAATAG	GGCATGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCCTCTT	GAECTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACCTG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAAGT	300
TGTCAATACT	ACCCGCTGG	TTTGCCTCCA	TCACATTGTT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTCCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACCTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACCTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCGACT	GTGCGGGACC	240

TGCAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCA	300
GAACCTTCCG CCTGTTCTCT GGCGTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG	360
ACCAGCGGAC AAACGGCGTT GAACAGCCGC ACCTCACGGA TGCCCCANTGT GTCGCGCTCC	420
AGGAACGGCN CCAGCGTGTC CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG ACCTTGCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC	60
AGTCCGAGCA GCCCCAGACC GCTGCCGCC GAAGCTAAGC CTGCCTCTGG CCTTCCCCTC	120
CGCCTCAATG CAGAACANT AGTGGGAGCA CTGTGTTAG AGTTAAGAGT GAACACTGTN	180
TGATTTTACT TGGGAATTTC CTCTGTTATA TAGCTTTCC CAATGCTAAT TTCCAAACAA	240
CAACAACAAA ATAACATGTT TGCCCTGTTNA GTTGTATAAA AGTANGTGAT TCTGTATNTA	300
AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTATTGG TNCTCTGGAA	360
ATAAAATATAT TATTAATAA	377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTGAGG GGTTAGGGTC CAGTTCCCAG TGGAAGAAC AGGCCAGGAG AANTGCGTGC	60
CGAGCTGANG CAGATTCCC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT	120
CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG	180
GAAGGCCCA TTCCGGGCT GTTCCCCGAG GAGGAAGGGA AGGGGCTCTG TGTGCCCCCC	240
ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAAA	300
TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCAC TGGCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA	480
AAAAAAAANA AAAAAA	495

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATTGCC ACCACCTAGT GGATGTCATT TAGAACATT TTGCTTGCTC	60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATT	120
TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACTC AATATGAAAA CTATTNACT	180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTGT TCATACTGTA TTTATCAAGT	240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA	300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCCTTT GTAACCTCAC	360
TTGGTTATT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA	420
TTTANTTCAN TAATTCTTT CCTTGTTAC GTTAATTGT AAAAGAATGC AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT	60
GTGGTGAAAT TTCAAAATTA TATGTAACCTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT	180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNCGANAATG TTCTAGNTAT	240
AGCTGGATAC ATACNGTGGG AGTCTATAA ACTCATACCT CAGTGGGACT NAACCAAAAT	300
TGTGTTAGTC TCAATTCTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT	360
GCAGGTAATC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAGTN ACATCTCGT	420
TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA	60
AAATAATGCT GCAAACCTAA TGTTCCTTATG CAAAATGGAA CGCTAACATGAA ACACAGCTTA	120
CAATCGCAAA TCAAAACTCA CAACTGCTCA TCTGTGTAG ATTTAGTGTAA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATACTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTAA CGGACTTTGA	180
AGTGATTCAAG TTTCCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACACGC TGGTTATCTA GATGAGAACA GAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTGAATAA TCTTGACGCT CCTGAACCTG CTCCTCTGCG A	461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGGCGCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAC	GCAGGTGCAG	GTGGCCGCC				269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGAGATTAG	GGTTTCTTGC	CAAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATAACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACCTTAAT	CCATTTTTAT	TTCAAAATGT	CTACAAATT	AATCCCATTA	TACGGTATTT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGTGTT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTTAAGGAA	CTAAAATAAA	AAAAAACACT	300

CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTCACACGG GATCTTAAC TTTACTCACT TTGTTTATTT	420
TTTAAACCA TTGTTGGC CCAACACAAT GGAATCCCCC CTGGACTAGT	470

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACCA AGTTACCATT TTATTTTACT	60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATTG TTAGGAATTG GCTTAAAATC TGCTAAAGT	180
GAAAATCTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGAAAAC ATCCAATTG	240
ATTTTCTTG TCTTTAAAAT TATCTAATCT TTCCATTTTT TCCCTATTCC AAGTCAATTG	300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTCTCTAAA	360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTGAT ATTTCTACCT	420
ACGTTAATAA AATAGCATTG TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTATGT	480
CCATTTAGT CACTAAACGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAATC ATCTTCCAG CTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCATAT AGTTATATCA AGTACTACCT TGCATATTGA	240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTGTATCA AACCTTTATT	300
TTCATGCAAA CTAGAAAATA ATGTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT	360
CAAAACTGCT CAAATTGTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTAAATATC CAAAATAATT	480
AAAGGAACAT TTTTAGCCTG GGTATAATTA GCTAATTAC TTTACAAGCA TTTATTAGAA	540
TGAATTCACTA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTAT	TTTTATATTT	AAAATTCATA	60
GAAAAAGTGCC	TTACATTTAA	TAAAAGTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCAAA	ATACATTAAG	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAAG	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTTAATTTG	TGATGAATAT	300
GGGGTGTAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGGTGG	ATATGAGTTG	ACAAGTTCT	CTTTCTTCAA	TCTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTCTTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAAAAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTAGTC	AAGTTCTAT	TTTTATTATA	ATTAAGTCT	TGGTCATTTC	60
ATTATTAGC	TCTGCAACTT	ACATATTAA	ATTAAGAAA	CGTTTAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCT	CCAAGAGTG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGAACATTA	GTAAATT	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTGT	GGCTCTTGC	ACTTGTTC	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107;

CGCCATGGCA	CTGCAGGGCA	TCTCGGTCAT	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCCCTGGCTG	ACTTCGGGGC	GCGTGTGGTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGGG	CAAGCGCTCG	CTAGTGCTGG	ACCTGAAGCA	180
GCGCGGGGA	GCCGCCGTGC	TGCGGCGTCT	GTGCAAGCGG	TCGGATGTGC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTCATGG	AGAAACTCCA	GCTGGGCCCA	GAGATTCTGC	AGCAGGGAAAAA	300
TCCAAGGCCTT	ATTATATGCCA	GGCTGAGTGG	ATTGGGCCAG	TCAGGAAGCT	TCTGCCGGTT	360
AGCTGGCAC	GATATCAACT	ATTGGCTTT	GTCAAGGTGTT	CTCTCAAAA	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATGCC	CGCTGAATCT	CCTGGCTGAC	TTTGCTGGTG	GTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTCTTT	TGACCGCACA	CGCACTGACA	AGGGTCAGGT	540
CATTGATGCA	AATATGGTGG	AAGGAACAGC	ATATTTAACGT	TCTTTCTGT	GGAAAACCTCA	600
GAAATCGAGT	CTGTGGGAAG	CACCTCGAGG	ACAGAACATG	TTGGATGGTG	GAGCACCTTT	660
CTATACCACT	TACAGGACAC	CAGATGGGG	ATTCAATGGCT	GTTGGAGCAA	TAGAACCCCCA	720
TTTCTACGAG	CTGCTGATCA	AAGGACTTGG	ACTAAAGTCT	GATGAACCTTC	CCAATCAGAT	780
GAGCATGGAT	GATTGGCCAG	AAATGAAGAA	GAAGTTTGCA	GATGTATTTG	CAAAGAAGAC	840
GAAGGCAGAG	TGGTGTCAAA	TCTTGACGG	CACAGATGCC	TGTGTGACTC	CGGTTCTGAC	900
TTTTGAGGAG	GTTGTTCATC	ATGATCACAA	CAAGGAACGG	GGCTCGTTA	TCACCACTGGA	960
GGAGCAGGAC	GTGAGCCCCC	GCCCTGCACC	TCTGCTGTTA	AACACCCCCAG	CCATCCCTTC	1020
TTTCAAAAGG	GATCCTTCA	TAGGAGAAC	CACTGAGGAG	ATACTTGAAG	ATTGGATT	1080
CAGCCGCGAA	GAGATTTATC	AGCTTAAC	AGATAAAATC	ATTGAAAGTA	ATAAGGTAAA	1140
AGCTAGTCTC	TAACCTCCAG	GCCCACGGCT	CAAGTGAATT	TGAATACTGC	ATTTACAGTG	1200
TAGAGTAACA	CATAACATTG	TATGCATGGA	AACATGGAGG	AACAGTATTAA	CAGTGTCTTA	1260
CCACTCTAAT	CAAGAAAAGA	ATTACAGACT	CTGATTCTAC	AGTGATGATT	GAATTCTAAA	1320
AATGGTTATC	ATTAGGGCTT	TTGATTTATA	AAACTTGGG	TACTTATACT	AAATTATGGT	1380
AGTTATTCTG	CCTTCCAGTT	TGCTTGATAT	ATTGTTGAT	ATTAAGATT	TTGACTTATA	1440
TTTTGAATGG	GTTCTAGTGA	AAAAGGAATG	ATATATTCTT	GAAGACATCG	ATATACATT	1500
ATTTACACTC	TTGATTCTAC	AATGTAGAAA	ATGAGGAAAT	GCCACAAATT	GTATGGTGAT	1560
AAAAGTCACG	TGAAACAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1620
A						1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65          70          75          80

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Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85 90 95
 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
 100 105 110
 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
 115 120 125
 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
 130 135 140
 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
 145 150 155 160
 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
 165 170 175
 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
 180 185 190
 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
 195 200 205
 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCAGACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCCCTC	TGCATCGACT	TCATGGTTT	CACGGTGCGG	240

CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCTCGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCCAGTAT	GCCAACCTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCTGTC	TCGTGGCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTTGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCAGCGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCCACTTG	780
CGCCTCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGGCCGT	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTCTAACG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGTG	GAGCAGGGAGG	TCCAGCAGTG	TAGCCCGTGC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCCTTG	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTGCTCCT	AGAGTAAGGC	TCATCTGGG	CTCGGCCCTCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCCCTACA	CTGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACCGCG	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATT	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GGCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTGCCAG	GCCTACTCTG	TCTATGCCCTT	780
CATGATCAGT	CTTGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCAAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCCGC	ACCCCTGC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTACA	CGGATTCGT	GGCGAGGGG	CTGTACCAGG	GCCTGCCAG	1200

AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTT	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATT	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCCG	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGG	1500
GAAGCAGGTG	TTCCCTGCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCCT	ATATGGTGT	1860
TGCCGCAGGC	CTGGGTCTGG	TGCCATTAA	CTTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGGAGGC	TTCCAAGGGG	GTTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAACCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460
GTCCTGAGGG	GCAACACACA	AGAACCCAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGCT	2520
GATCCACCCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCTGT	TGGTCCCTCT	GTTGCCATCA	2580
CAGAGACACA	GGCATTAAA	TATTTAACCTT	ATTTATTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTTT	TCTGTGTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCCCC	AAAATGCTA	ACCCAGGACC	TTGAAATTTC	TACTCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGCCCAG	CCTGGTTCCC	CCCACTTCCA	2940
CTCCCTCTA	CTCTCTCTAG	GACTGGGCTG	ATGAAGGCAC	TGCCCAAAAT	TTCCCCCTACC	3000
CCCAACTTT	CCCTACCCCC	AACTTCCCC	ACCAGCTCCA	CAACCCCTGT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAAG	TGCGGTTTCC	CAAGCCTTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTGC	TTGGGGATC	TCACACAGAA	ACTCAGGAGC	ACCCCTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTAAGT	GCGGTTGCA	ATAATGTCGT	CTTATTATT	3240
TAGGGGGTG	AATATTTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAARA	AAAAAAAARA	AAAAAAAARA	AAAAAAATAA	AAAAAAAATAA	AAAAAAAATAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCCT	CCCTCTGCCT	GCCCCACTCAG	TGGCACACACC	CGGGAGCTGT	TTTGTCTTT	60
GTGGAGCCTC	AGCAGTTCCC	TCTTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGGAGCCA	120
CCATGCAGTG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCATTTG	CTCATCTTC	180
TGTGTGGTGC	AGCCCTGTTG	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTC	240
TGAAGATCTT	CGGGCCACTG	TCGTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300

TCATCGCAGC	CGGCGTTGTG	GTCTTGCCTC	TTGGTTCCCT	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCCT	CCTCCTCATC	TTCAATTGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCCTGACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCTA	GGAAGACTTC	ACTCAAGTGT	540
GGAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATAACG	GATTTGAGG	600
ACTCACCCCTA	CTTCAAAGAG	AACAGTGCCT	TTCCCCCATT	CTGTTGCAAT	GACAAACGTCA	660
CCAACACAGC	CAATGAAACC	TGACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTGTAT	GACATCCGAA	CTAATGCAGT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACTTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAAC	GTGAAGAGGC	900
ACCCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCAC	CCTTTAGCG	1020
ATGCCTGACT	TTCCCTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCCTAGGCC	1140
TAGTGGTGTAT	CCCAGTGCTC	TACTGGGGA	TGAGAGAAAG	GCATTTATA	GCCTGGGCAT	1200
AAGTGAAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACTTCAAAAA	TGCATAAAACC	1260
TGTTACAATG	TTAAAAAAAAA	AAAAAAAAAA				1289

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
 20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
 85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
 100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
 115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe

130	135	140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys		
145	150	155
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu		
165	170	175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln		
180	185	190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu		
195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
		15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20	25	30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Glu Val Gly Val		
35	40	45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val

20	25	30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser		
35	40	45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly		
50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCTC	TCCCCTCCCTC	TGAATTAAAT	TCTTCAACT	TGCAATTGCG	AAGGATTACA	60
CATTCAC TG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTG	TTAAAATTAC	120
TTGGTTTG	AATCCATCTT	GCTTTTCCC	CATTGGA	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAAC	ATTTCACCCA	GACAGCCTGT	TTCTATCCTG	TTAATAAAAT	TAGTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
					TTAGTC	366

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCT	ATATTATAGC	AAAATAAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTCATAT	TTTAAGACAC	ATGATTATC	CTATTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCT	TT		282

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGAA	ACAGATGAGG	TCACCTCTGT	240
GAECTGCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTCAGAC	AGGGAGAAAT	300
					TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAAATC TGAGTGGAAA	60
AANTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCAAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCAGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAG T	171

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATT TT ATTCTCTTGG	120
TTAACAGATTTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCAC TGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCTCTCAC AACACAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAAACCTC AGTGCCTCTC	420
CTCTTGCCT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAAATT GT	112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG 54

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCCTCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT	240
TTCCTGCAAA AGGCTCACTC AGTCCCTTG C TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCAA ATCATTCACTC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA	TGGAATGAGT	AGACTGTATG	TTTGAANATT	TANCCACAAAC	CTCTTGACA	60
TATAATGACG	CAACAAAAAG	GTGCTGTTA	GTCCTATGGT	TCAGTTTATG	CCCCTGACAA	120
GTTCATTG	TGTTTGCCG	ATCTTCTGGC	TAATCGTGGT	ATCCTCCATG	TTATTAGTAA	180
TTCTGTATTG	CATTTGTTA	ACGCCTGGTA	GATGTAACCT	GCTANGAGGC	TAACTTATA	240
CTTATTAAA	AGCTCTTATT	TTGTGGTCAT	AAAATGGCA	ATTATGTGC	AGCACTTATG	300
TGCAGCAGGA	AGCACGTGTG	GGTTGGTTGT	AAAGCTCTT	GCTAATCTTA	AAAAGTAATG	360
GG						362

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA	GATCGTGTCC	ACTCCTGTGG	ACATCTGTT	TTAATGGAGT	TTCCCATGCA	60
GTANGACTGG	TATGGTTGCA	GCTGTCCAGA	TAAAAACATT	TGAAGAGCTC	CAAATGAGA	120
GTTCTCCAG	GTTCGCCCTG	CTGCTCCAAG	TCTCAGCAGC	AGCCTCTTTT	AGGAGGCATC	180
TTCTGAACTA	GATTAAGGCA	GCTTGAAAT	CTGATGTGAT	TTGGTTTATT	ATCCAACCAA	240
CTTCCATCTG	TTATCACTGG	AGAAAGCCA	GACTCCCCAN	GACNGGTACG	GATTGTGGGC	300
ATANAAGGAT	TGGGTGAAGC	TGGCGTTGTG	GT			332

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
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AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTG TATCTCGGGT	180
TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAACAGTTG	240
GGATGCTTCT AAAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTAA CCAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTCCCCC TTTCCATCTG GCTCCTGGGT TGACAATTG TGAAACAAAC TCTATTGCTA	120
CTATTTAAAA AAAATCACAA ATCTTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCTG	180
CTATTCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAAACA	60
TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTT TACTTGTATT TTGCTTTGG	120
T	121

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC	ATGCCTAGCA	CATCAGAATC	CCTCAAAGAA	CATCAGTATA	ATCCTATAACC	60
ATANCAAGTG	GTGACTGGTT	AAGCGTGCAG	CAAAGGTCAG	CTGGCACATT	ACTTGTGTGC	120
AAACTTGATA	CTTTTGTCT	AAGTAGGAAC	TAGTATACAG	TNCCTAGGAN	TGGTACTCCA	180
GGGTGCCCG	CAACT CCTGC	AGCCGCTCCT	CTGTGCCAGN	CCCTGNAAGG	AACTTCGCT	240
CCACCTCAAT	CAAGCCCTGG	GCCATGCTAC	CTGCAATTGG	CTGAACAAAC	GTTTGCTGAG	300
TTCCCAAGGA	TGCAAAGCCT	GGT GCTAAC	TCCTGGGGCG	TCAACTCAGT		350

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA	AGACGACAGA	AGTTGCATGG	CAGGGACAGG	GCAGGGCCGA	GGCCAGGGTT	60
GCTGTGATTG	TATCCGATA	NTCTCGTGA	GAAAAGATAA	TGAGATGACG	TGAGCAGCCT	120
GCAGACTTGT	GTCTGCCTTC	AANAAGCCAG	ACAGGAAGGC	CCTGCCTGCG	TTGGCTCTGA	180
CCTGGCGGCC	AGCCAGCCAG	CCACAGGTGG	GCTTCTTCCT	TTTGTGGTGA	CAACNCCAAG	240
AAAAC TGCAG	AGGCCAGGG	TCAGGTGTNA	GTGGGTANGT	GACCATAAAA	CACCAGGTGC	300
TCCCAGGAAC	CCGGGCAAAAG	GCCATCCCCA	CCTACAGCCA	GCATGCCAC	TGGCGTGATG	360
GGTGCAGANG	GATGAAGCAG	CCAGNTGTT	TGCTGTGGT			399

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGTGA	TGCTGGTGGT	ANAAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTTGGCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGTT	CCTGT		165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTAAGAACAT	TAATGGCTCC	60
TTAACTTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGAAAC	GTTAACAGCC	ACATGCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAGGTGC	TTGGGGTGG	GGGCTGGGG	CATANANGGT	240
CANGCTCAG	GAAGCCTCAA	GTTCCATTCA	GCTTGCCAC	TGTACATTCC	CCATNTTTAA	300
AAAAACTGAT	GCCTTTTTT	TTTTTTTTG	AAAAATTC			338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTGGCA	TCTGGTTGC	CTATAGCCGA	GGCCACTTTG	ACAGAACAAA	60
GAAAGGGACT	TCGAGTAAGA	AGGTGATTAA	CAGCCAGCCT	AGTGCCCGAA	GTGAAGGAGA	120
ATTCAAACAG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACCGCC	TATCATCTGC	180
ATTTGCCTTA	CTCAGGTGCT	ACCGGACTCT	GGCCCCGTAT	GTCTGTAGTT	TCACAGGATG	240
CCTTATTGTTG	CTTCTACACC	CCACAGGGCC	CCCTACTTCT	TCGGATGTGT	TTTTAATAAT	300
GTCAGCTATG	TGCCCATCC	TCCTTCATGC	CCTCCCTCCC	TTTCCTACCA	CTGCTGAGTG	360
GCCTGGAACT	TGTTAAAGT	GT				382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT	CTTTCTGTTG	TGTTNGATTT	TACTATAGGG	GTTTNGCTTN	TTCTAAANAT	60
ACTTTTCATT	TAACANCTT	TGTTAAGTGT	CAGGCTGCAC	TTTGCTCCAT	ANAATTATTG	120
TTTTCACATT	TCAACTTGTA	TGTGTTGTC	TCTTANAGCA	TTGGTGAAAT	CACATATTAA	180
ATATTTCAGCA	TAAAGGGAGAA					200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTGGTGG	60
GGGTGCTGAC TAAACTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGTGA	180
AATGGTTCTG AGAACCATCC AATTACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTTCAAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATTT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAAACAGA CGTGTATTTA	60
GGGTTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCAAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTTG TTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTG TATTGTAAT GGCAAACATC CAGNAGCAAT TCCTAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCC TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAGT GGCTCTGAC	TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT	TGCTCTGGTT GGTTGAGAGA GCTCCTTGCGAACAGGCCT	120
CCAAGTCAGG GCTGGGATTG	TTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA	TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCTT	CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG	CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT	TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT	CTTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT	TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCTT TATCTCATCG AATTTTAAC CCAAACCTCAC	TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT	ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATT	CCTTCCTGTC CTGACCCTGAGCCATTGGG	180
GTTGGCCTTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC	CCTTGAGCTC CATTGCTCAC	240
NCCANCCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC	CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAGT TACTATTAAC	ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC	ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCCTTAA	TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAAATAAAC TTGCAATGAG AGCATTTAAG AGGAAAGAAC	60
TAACGTATTT TAGAGGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACAA	180
TTTCAGGCAG AGGAAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGGG T	111

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAC	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCTTT TCATCTAGTG GTGAAACCT GATGCTTAT GTTGACAGGA ATAGAACAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTCA	60
CTTCTGCTCT TATGTCCTCA TCTGACACT CTTTACCAT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCTTAAAT TATCTTAAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAACGCCG TTACACAGCT AACTCCCCTT GGCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCTCT GAAATAAAAT CCGGAGAATG	300

GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG

333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG	60
GAAAGTGCCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTGGCT	240
GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTAGGCATGCTG	300
GCCCTGGT	308

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTAGACAT TTAGTTGAAG ATTTCCTACA CAGGAACATGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGTA TATCTGTCCC	120
CTTAGT	126

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCACTCCTT CCTTCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGTAA TTCACCATA ATTTCCTCCC CCAAACCTCTC TGAGTCTTC CTTAATATTT	180
CTGGTGGTTC TGACCAAAGC AGGTCACTGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATTTTGTA GCCTTGACATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCCCTGT TTTCCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGG	360
NACAGACGGG CTCTTGACAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTCCT CTGATGTCCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTC	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGCGGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC	240
TGCTGTGGTG CCGGGGAGNTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGTTGTG GGAGCTGGCA NGGGTCANTG TTGTGTGTAA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTGN	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCAAC	480
AAGGGAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC	240
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTG TAACATCCTG	300
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAAA	60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATAACA GACAGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTTAAT GAGGGAGTTC CAGGAGATTG AACCAAGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAACGT CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
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ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CGGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAAG TGTGCTCAAT CTTGGGCTTG GCGCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTGCCA CAAGCTTCCC AGGCTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCCCT ACCACACAAA AACAAATAGGA TCACTGCTGG GCACCCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA	TCATAAACGG	CGAGGACTGC	AGCCCGCACT	CGCAGCCCTG	GCAGGGCGCA	60
CTGGTCATGG	AAAACGAATT	GTTCTGCTCG	GGCGTCTCTGG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGCAC	ACTGTTCCA	GAAGTGAGTG	CAGAGCTCCT	ACACCATCGG	GCTGGGCCTG	180
CACAGTCTTG	AGGCCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTACAACAG	ACCCCTTGCTC	GCTAACGACC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTGT	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCTACC	360
GCAGGGAACT	CTTGCCTCGT	TTCTGGCTGG	GGTCTGCTGG	CGAACGGCAG	AATGCCTACC	420
GTGCTGCAGT	GCGTGAACGT	GTCGGTGGTG	TCTGAGGAGG	TCTGCAGTAA	GCTCTATGAC	480
CCGCTGTACC	ACCCCAGCAT	GTTCTGCGCC	GGCGGAGGGC	AAGACCAAGAA	GGACTCCCTGC	540
AACGGTACT	CTGGGGGGCC	CCTGATCTGC	AACGGGTACT	TGCAGGGCCT	TGTGTCTTTC	600
GGAAAAGCCC	CGTGTGGCCA	AGTTGGCGTG	CCAGGTGTCT	ACACCAACCT	CTGCAAATTC	660
ACTGAGTGGA	TAGAGAAAAC	CGTCCAGGCC	AGTTAACTCT	GGGGACTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCTCCT	780
CCCTCAGGCC	CAGGAGTCCA	GGCCCCCAGC	CCCTCCTCCC	TCAAACCAAG	GGTACAGATC	840
CCCAGCCCC	CCTCCCTCAG	ACCCAGGAGT	CCAGACCCCC	CAGCCCCCTCC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCTCCT	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCCTCCTCC	960
CTCAGACCCA	GGGGTCCAGG	CCCCCAACCC	CTCCTCCTC	AGACTCAGAG	GTCCAAGCCC	1020
CCAACCCNTC	ATTCCCCAGA	CCCAGAGGTC	CAGGTCCCAG	CCCTCNNTCC	CTCAGACCCA	1080
GCGGTCCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGCC	CCCTTGTGGC	ACGTTGACCC	1140
AACCTTACCA	GTTGGTTTT	CATTTTNGT	CCCTTCCCC	TAGATCCAGA	AATAAAGTTT	1200
AAGAGAAGNG	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1															15

Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
															20
															25

Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly		
50	55	60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu		
65	70	75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe		
85	90	95
Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser		
100	105	110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe		
115	120	125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn		
130	135	140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		
145	150	155

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCC	GCACGGTCA TGGAAAACGA ATTGTTCTGC	60
TCGGGCGTCC TGGTGATCC GCAGTGGGTG	CTGTCAGCCG CACACTGTT CCAGAACTCC	120
TACACCATCG GGCTGGCCT GCACAGTCTT	GAGGCCGACC AAGAGCCAGG GAGCCAGATG	180
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA	GAGTACAACA GACCCTTGCT CGCTAACGAC	240
CTCATGCTCA TCAAGTTGGA CGAATCCGTG	TCCGAGTCTG ACACCATCCG GAGCATCAGC	300
ATTGCTTCGC AGTGCCTTAC CGCGGGGAAAC	TCTTGCCTCG TTTCTGGCTG GGGTCTGCTG	360
GCGAACGGTG AGCTCACGGG TGTGTGTCTG	CCCTCTTCAA GGAGGTCCCT TGCCCAGTCG	420
CGGGGGCTGA CCCAGAGCTC TGCCTCCCAG	GCAGAAATGCC TACCGTGCTG CAGTGCCTGA	480
ACGTGTCGGT GGTGTCTGAG GAGGTCTGCA	GTAAGCTCTA TGACCCGCTG TACCACCCCA	540
GCATGTTCTG CGCCGGCGGA GGGCAAGACC	AGAAGGACTC CTGCAACGGT GACTCTGGGG	600
GGCCCCTGTAT CTGCAACGGG TACTTGCAGG	GCCTTGTGTC TTTCGGAAAA GCCCCGTGTG	660
GCCAAGTTGG CGTGCCAGGT GTCTACACCA	ACCTCTGCAA ATTCACTGAG TGGATAGAGA	720
AAACCGTCCA GGCCAGTTAA CTCTGGGAC	TGGGAACCCA TGAAATTGAC CCCCAAATAC	780
ATCCCTGCGGA AGGAATTCAAG GAATATCTGT	TCCCAGCCCC TCCTCCCTCA GGCCCAGGAG	840
TCCAGGCCCC CAGCCCCCTCC TCCCTCAAAC	CAAGGGTACA GATCCCCAGC CCCTCCCTCCC	900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC	CTCCTCCCTC AGACCCAGGA GTCCAGCCCC	960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC	CCAGCCCCCTC CTCCCTCAGA CCCAGGGTT	1020
GAGGCCCTCA ACCCCTCCTC CTTCAGAGTC	AGAGGTCCAA GCCCCCAACC CCTCGTTCCC	1080
CAGACCCAGA GGTNNAGGTC CCAGCCCCCTC	TTCCNTCAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTCC CTGNACACAG TGCCCCCTTG	TGGNANGTTG ACCCAACCTT ACCAGTTGGT	1200

TTTTCATTT TNGTCCCTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAA AAAAAA	1260 1265
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(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC ACACGTGTT CAGAAAGTGAG TGCAGAGCTC CTACACCATC GGGCTGGGCC	60
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG	120
TACGGCACCC AGAGTACAAC AGACCCCTTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG	180
ACGAATCCGT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTGCTTCG CAGTGCCCTA	240
CCGCGGGGAA CTCTTGCTC GTTCTGGCT GGGGTCTGCT GGCGAACGGT GAGCTCACGG	300
GTGTGTGTCT GCCCTCTTCA AGGAGGTCTCT CTGCCCAGTC GCGGGGGCTG ACCCAGAGCT	360
CTGCGTCCCA GGCAGAAATGC CTACCGTGCT GCAGTGCCTG AACGTGTCGG TGGTGTCTGA	420
NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACCACCCCC ANCATGTTCT GCGCCGGCGG	480
AGGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGG AAAGGGGAGG GCAGGGCACT	540
CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CGCGATGGCG AGATGCAGAG	600
ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AACTGAGAG AAACAGAGAA	660
ATAAACACAG GAATAAAAGAG AAGCAAAGGA AGAGAGAAAC AGAAACAGAC ATGGGGAGGC	720
AGAAACACAC ACACATAGAA ATGCAGTTGA CCTTCCAACA GCATGGGGC TGAGGGCGGT	780
GACCTCCACC CAATAGAAAA TCCTCTTATA ACTTTTGACT CCCCAAAAAC CTGACTAGAA	840
ATAGCCTACT GTTGACGGGG AGCCTTACCA ATAACATAAA TAGTCGATTG ATGCATACGT	900
TTTATGCATT CATGATATAC CTTTGTGGT ATTGTTTGAT ATTCTTAAGC TACACAGTTC	960
GTCTGTGAAT TTGTTAAAT TGTTGCAACT CCTCCTAAAT TTGTTCTGATG TGTTTATTGA	1020
AAAAATCCAA GTATAAGTGG ACTTGTGCAT TCAAACCAAGG GTTGTTCAG GGTCAACTGT	1080
GTACCCAGAG GGAAACAGTG ACACAGATT ACAGAGGTGA AACACGAAGA GAAACAGGAA	1140
AAATCAAGAC TCTACAAAGA GGCTGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTTT	1200
GGGAGGCGAG GCAGGCAGAT CACTTGAGGT AAGGAGTTCA AGACCAGCCT GGCCAAAATG	1260
GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCCTGT	1320
AATCCCAGCT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT	1380
GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGC AACAGAGTAA GACTCTGTCT	1440
CAAAAAAAAAA AAAAAAAAAA	1459

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGG	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GAECTCTGCA	ACGGTGACTC	TGGGGGGCCC	CTGATCTGCA	ACGGGTAATT	GCAGGGCCTT	540
GTGTCTTCG	GAAAAGCCCC	GTGTGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCCA	720
GCCCCCTCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCCTC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTCCCTCT	AGATCCAGAA	1140
ATAAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10						15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20 25 30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35 40 45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCAGTG	GTCATGGAAA	ACGAATTGTT	CTGCTGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTCAGGAA	CTCCTACACC	120
ATCAGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCC	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACCTTTGC	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCCCTGGC	AGGGTTGTAC	CATTTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480
CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGGAA	CACTGTGATC	AACTAGCCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTG	TGTCTATTGT	600
ACTAACCATG	CCGATGTTA	GGTGAATT	GCCTCACCTG	GCCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTTCTG	CTTCAGTGTG	AGCCATTCCC	ACATAATTTC	720
TGACCTACAG	AGGTGAGGGA	TCATATAGCT	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCATTTCTC	CTGTTGTAGT	GAAAGGTGCG	CCCTCTGGAG	CCTCCCAGGG	TGGGTGTGCA	840
GGTCACAATG	ATGAATGTAT	GATCGTGTTC	CCATTACCCA	AAGCCTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTTC	TTCAAGGAT	GTATGCTGTC	CATTGATGCA	960
ACCACCTCAG	GACTCCTGGA	TTCTCTGCCT	AGTTGAGCTC	CTGCATGCTG	CCTCCTTGGG	1020
GAGGTGAGGG	AGAGGGCCA	TGGTTCAATG	GGATCTGTG	AGTTGTAACA	CATTAGGTGC	1080
TTAATAAACAA	GAAGCTGTGA	TGTTAAAAAA	AAAAAAAAAA			1119

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100 105 110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115 120 125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130 135 140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
 145 150 155 160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC	TTGGTGTTC	AAGCCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CCGGCCGGGG	GATGCGAGGC	TCGGAGCACC	CTTGCCTCGC	TGTGATTGCT	120
GCCAGGCACT	GTTCATCTCA	GCTTTCTGT	CCCTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTTCATAT	CTGGAGCCTG	ATGTCTAAC	GAATAAGGT	CCCATGCTCC	ACCCGAAAAAA	240
AAAAAAAAAAA						250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTAACA	60
TCACCCAGAC CCCGCCCTG CCCGTCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTG TATAAATGCC	180
TGATTTAAAAA AAAAAAAA AA	202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTGKT NAGGTTKKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTCTGAA GATTAATGAA GTGAAAATT GAGGTGGATA AATACAAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTT GGGAGCCAA	360
ATTGATAATA TTCTATGTT TAAAAGTTGG GCTATACATA ATTATTAAG AAATATGGAW	420
TTTATTCCC AGGAATATGG KGTTCATTT ATGAATATTA CSCRGGATAG AWGWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC	540
CAAAAAAAA AAAAAAAA	558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTTGA TCCAACCCTG GCTTWTTTTC	60
AGAGGGGAAA ATGGGGCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTG ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGTT GATAGGAANT	360
NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTG TGACGCATARA	420
AWTGSTGARA AAATTAAAAT GTTCTGGTT MACTTAAAAA ARAAAAAAAA AAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC	AGAACGCTAAA	GCCAAAGCCC	AAGAACAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAAGTA	CCAATAACAG	TGCCAGTGCC	AGTGCCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTGCCAGCC	TGACCGCCAC	TCTCACATT	GGGCTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTTAGATAT	240
TGTTAACCT	GCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCAGAAAC	CTACTCAACA	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATT	360
GCCATTCAA	AAAAAAA	AAAAA				384

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG	GACCCTGGC	TTATAAGCGA	TCATGTYNT	CCRGTATKAC	CTCAACGAGC	60
AGGGAGATCG	AGTCTATAACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AAACGTTCAA	GGTGCTCATG	ACCCAGCAAC	CGGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTT	TCTGCCACCT	GTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTG	CCAGCCATAC	TCTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAATT	ACTACMAGAW	TATTWMAW	WAAATGAWTT	GAAAAACTST	480
TAAAAAAA	AAAAA					496

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT	GCGCSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTCGGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGCTGCT	CCTCGTCATC	TTCTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360

GCGCAGCGTT ACCGCCTCAT CCGG

384

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTGCCACCA	CYTCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCCTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAAG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCTGAA	GARCAACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAG	ACATTGACAA	ACTCGCCCAG	420
GTGGAAAAAG	AMCAMCTCCT	GGARGTGCTN	GCGCCTCCTC	GTCMGTGTTG	GGCAGCGCTW	480
TCCTTTTGAC	ACACAAACAA	GTAAAGGCA	TTTCAGCCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAT			577

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTA	AGCCTGGACA	CTGGTATTAA	AATTACAAT	ATGCAACACT	120
TTAACACAGTG	TGTCAATCTG	CTCCCCYNNAC	TTTGTATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTG	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAAAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGGA	GCGGAAGAGT	AGCCTTTCTA	CTTCACCAGA	CACAACCTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTG	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAAGT	ATCTCTAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATTTTT	TACTTTGTA	AAAGCTTATG	120

CCTCTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTTCCTCC	420
GCAAAAAACA	TGTACNGACT	TCCCAGTGGAG	TAATGCCAAG	TTGTTTTTT	TATNATAAAA	480
CTTGCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	ATAAGCAGT	GTGCCTAAC	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTCATTA	TAAATGTTG	CTAAAATACA	CTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTA	GATTATGT	AGTATNAAGT	GAAAANTAC	720
GAAAATAATA	ACATTAAGA	AAAANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180
AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTGGCT	NGTCATNGAA	NGGGCANTTT	TCCAANTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTT	TTTAAACACA	GTTCATCACA	ACAAAATT	TTAGAAGAAT	AGTGGTTTG	60
AAAACCTCTG	CATCCAGTGA	GAAC	ACACCACATT	ACAGCTNGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAAG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAA	AGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	AGAACTGCNT	300
TGAAAATTT	CATGTATGCA	ATCCAACAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATTTNNNT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTT	TASTGTCGGM	CTGTTCA	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120
ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTGATTC	AGTTAGTATA	AGCTCTCCA	180
CTTCCTTGT	TAAGACTTCA	TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC	300
CTTTGTGCAT	CCATTAAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAAATTCTGC	360
AAGAGTCATC	TGTCTGCAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAAACACACYT	CCATCCCGBT	180
CTTTGTGGA	AAAAGTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCATT	GCTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTGTTT	CAAAAGCARC	TCTTGGTGCC	420
TGTTGGATCA	GGTCCCATT	TCCCAGTCYG	AATGTTTCACA	TGGCATATT	WACTTCCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGAACAG	CAAATCTGT	TCCGGCAT	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCAGAACAG	GCGCGTGAG	CCCCACCAGC	AGCAGAACGA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 608 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GAATCTCCAC	CTGCTGGAAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCTTGC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GGCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCAGTG	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGGCAGC	ATGAAGGCAGT	TGTCGGCTCG	CAGTTCTCT	TCAGGAACTC	600

CACGCAAT

608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGTATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCACAAAC	240
AACAACAAACA	AAATAACATG	TTTGCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACACAS	TTCTGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCCTCC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNNG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAAA	AAAAANAAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCAT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300

ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTGTA	360		
TCACTTGGTT	ATTTTATTGT	AAATGARTTA	CAAATCCTT	AATTTAAGAR	AATGGTATGT	420		
WATA	TTTATT	TCATTA	TTT	CTTCCTKGT	TTACGTWAAT	TTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTTT	540		
TTCTT	AGAAT	GTATAAAGGT	TGTAGCCC	CNAACTCAA	AGAAAAAAAT	GACCACATAC	600	
TTTGCAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660		
						AAGTG	665	

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTTGC	AGGAAGGATT	CCATTATTG	TGGATGCATT	TTCACAATAT	60	
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120	
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180	
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAAT	CCAAACTGAA	240	
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300	
ATTCTCTTCT	GAACTTAGA	TTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360	
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420	
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATT	GTTCATNCTG	480	
						ANCNTGGCTT AA	492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTG	ATTTCANTCT	GTANNAANTA	TTTCATTAT	TTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

ACTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCACGTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAG TTTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCNAC TCTAACACG CTGGTTATCT NAGATGAGAA NCAGAGAAAAT AAAGTCNAGA	300
AAATTACCT GGANGAAAAG AGGCTTNNGG CTGGGGACCA TCCCATTGAA CCTTCTCTTA	360
ANGGACTTTA AGAANAAAAT ACCACATGTN TGTNGTATCC TGGTGCCNNGG CCGTTTANTG	420
AACNTNGACN NCACCCTTNT GGAATANANT CTTGACNGCN TCCTGAACCTT GCTCCTCTGC	480
GA	482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGT GAANGCGGGG GGCCTCGGGG AGCCCCTCGG GAAGGGCGGC	240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC	270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT TTTTGGAAATC TACTGCGAGC ACAGCAGGTC AGCAACAAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCAAG GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAAGC ANAANTAAACA	180
TGGAGTGGGT GCACCCCTCCC TGTAGAACCT GGTTACNAAA GCTTGGGGCA GTTCACCTGG	240
TCTGTGACCG TCATTTCTT GACATCAATG TTATTAGAAG TCAGGGATATC TTTTAGAGAG	300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCAANA TCCAANAAA ATCCACNTGA	360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATAACNG	120
GTNATTTC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAACAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTAA	CACTGCAAAC	ATNTTNNAA	300
GGAACAAAAA	TAAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAACAAACAA	ATTCAACNG	360
CAACANCNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAA	TTTACTNCA	CTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAACAA	480
CAATGGNAAT	NCCNCCNCG	TGGACTAGT				509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTGA	CCCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAA	GGCAGCTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGAAACAC	ATCCAAATT	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCATTT	300
GCTTCTCTAG	CCTCATT	TAGCTTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTCTACC	420
TACGTTATA	AAATAGCATT	TTGTGAAGCC	AGCTCAAAG	AAGGCTTACA	TCCTTTATG	480
TCCATT	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAGGTTT	GTGACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATTTTC	CAGCTTAAA	ATAACAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTCTCC	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	TCAAACCTTT	300
ATTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTCAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCAAG	TTAAATATCC	480
AAAATAATTA	AAGGAACATT	TTTAGCCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTACACA	TGTTTATTATT	CCNTAGCCC	ACACAATGG		589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATTAA	TTTTTATATT	TAAAATTCA	60
AGAAAAGTGC	CTTACATTAA	ATAAAAGTTT	GTTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTGAAGAAGA	AAAATTGTA	CCTCAGAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGTGTC	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTCT	TCAATCTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TTGCCAATAT	TAAAAAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTAGTC	AAGTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATT	60
CATTTATTAG	CTCTGCACT	TACATATTAA	AATTAAAGAA	ACGTTNTTAG	ACAACGTNA	120
CAATTTATAAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATTC	TCTTCTCCAT	CCCCATGTNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGCTT	360
TCCGTGAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTANAA	CTAGCAACTC	TTATTCTTT	CCTTTAAAAA	60
TACATAGCAT	AAAATCCCAA	ATCCTATTAA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTCTGG	TGGTTCTGCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTGCAAT	GCAGAGGAGG	TAAGAGGTAT	TGGATTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300

AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA

332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTCC	GGCCCCATCC	AACCACGAAG	TTGATTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCTGA	TTCACATTAA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAATACT	240
TTTGGCAGAA	TACTTNTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCACAAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAATTAA	CCTGTTACAA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCAAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCAACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATT	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCCAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAACTGCC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTTGA	GGGACTAAATG	GAAAAACGTA	120
TGGGGAGATT	TTANCCAATT	TANGTNTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAAATGGGAN	GGCTGGTTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTG AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA	60
GGATTTAATG TTGTCCTCAGC TTGGGCACCT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG	180
TTNAATTTC TTCCCATGTA CTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCTTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGCCACA	300
TTTTTTTTTC CTTTATTCTT TTGTCAGA	328

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACGTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTTG	ATTGTCAAAG	60
GATTAAATGT	TGTCTCAGCT	TGGGCACTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAGCGC	GACAACAGGT	TATTGAACCTT	GCCCCCCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCACAT	300
TTTTTTTCTC	TTTATTCTCTT	TGTAGAGAT	GCGATTATC	CATATGCTAN	AAACCAACAG	360
AGTGACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTGCTCT	CCCTAATATA	CCTC				444

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCCACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCAGGT	TTCCAACCAA	GGTGGAAATC	TCCTATACTT	360
GGTGCC						366

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAACAT	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNNTAA	GGGCTNTTNC	ATTTTTTTAT	120
TAATAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240
AATTCTTCCT	TCCCTCCTTT					260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTCAAGGAA NAGGAACGCA TATAATTGTA	60
TCTTCCTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCC	240
ATATCCTTCA TGCTTGTAAA GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACACACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTA AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	60 93
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(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGGA TTCCATGAGG TCTTTGCCA AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	60 120 167
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(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC GTTCTTCACC TGTCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA ATGTTTGCTG AATTAAAGGA TGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA TTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAACTTT TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	60 120 180 240 300 351
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(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT TGGTAATTAT GGTCAATTAA ATWRTRTTKT GGGGCATTTC CTTACATTGT CTTGACAAGA TTAAAATGTC TGTGCCAAA TTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG TGTGCTATT TAAAAGATT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAAT CTTTATTGC ACTTGTGTTG ACCATTAAGC TATATGTTA AAA	60 120 180 240 300 360 383
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(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGT	TA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG	TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA	RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR	AAATGGAAGC CCTTAAAGGT GCTTGATAAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC	CTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM	GCATTGTGAC	320

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CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
(a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;

(b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:
(a) obtaining a biological sample from the patient;
(b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and

(c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a

sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a

polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific

for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences

recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

U S P A T E N T
P R I O R I T Y
D A T E
A P P L I C A T I O N
N U M B E R
F I L E D
O F F I C E
O F P A T E N T
A N D
T R A D E
M A R K S
O F F I C E
U S P A T E N T
P R I O R I T Y
D A T E
A P P L I C A T I O N
N U M B E R
F I L E D
O F F I C E
O F P A T E N T
A N D
T R A D E
M A R K S
O F F I C E

COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

ABSTRACT OF THE DISCLOSURE

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jiangchun Xu and Davin C. Dillon
Filed : February 25, 1998
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CANCER AND METHODS FOR THEIR USE
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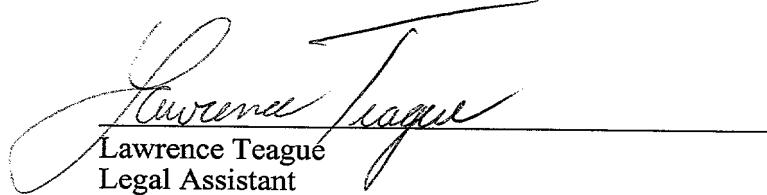
DECLARATION

Sir:

I, Lawrence Teague, in accordance with 37 C.F.R. § 1.821(f) do hereby declare that, to the best of my knowledge, the content of the paper entitled "Sequence Listing" and the computer readable copy contained within the floppy disk are the same.

I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated this 25th day of February, 1998.



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